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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:52:02 ; Search time 19.29 Seconds
(without alignments)
723.227 Million cell updates/sec

Title: US-09-442-143-4
Perfect score: 2340
Sequence: 1 MRLPGWLWSSAVLACRAV.....GYKSSFKQAKMIRPKFKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2340	100.0	432	1 FIBX_MOUSE	P12804 mus musculus
2	493.5	21.1	463	1 FIBX_CHICK	Q02020 gallus gall
3	488.5	20.9	437	1 FIBG_HUMAN	P02679 homo sapien
4	488.5	20.9	453	1 FIBH_HUMAN	P04469 homo sapien
5	470.5	20.1	477	1 FIBB_PETMA	P02678 petromyzon
6	466	19.9	444	1 FIBG_BOVIN	P12799 bos taurus
7	463.5	19.8	282	1 FIBG_FARPA	P19477 parastichop
8	463	19.8	491	1 FIBB_HUMAN	P02675 homo sapien
9	459	19.6	468	1 FIBB_BOVIN	P02676 bos taurus
10	454	19.4	866	1 FIBH_HUMAN	P02671 homo sapien
11	452	19.3	782	1 FIBR_RAT	P06399 rattus norv
12	448.5	19.2	438	1 FIBG_XENLA	P17634 xenopus lae
13	444	19.0	479	1 FIBG_RAT	P14480 rattus norv
14	435	18.6	445	1 FIBG_RAT	P02680 rattus norv
15	431.5	18.4	741	1 FIBR_CHICK	P14448 gallus gall
16	426.5	18.2	432	1 FIBG_PETMA	P04115 petromyzon
17	417	17.8	255	1 MFA4_HUMAN	P55083 homo sapien
18	416.5	17.8	1808	1 TENA_CHICK	P10039 gallus gall
19	414.5	17.7	4289	1 TENX_HUMAN	P22105 homo sapien
20	408.5	17.5	1746	1 TENA_PIG	Q29116 sus scrofa
21	406.5	17.4	2201	1 TENA_HUMAN	P24821 homo sapien
22	377	16.1	641	1 FIB2_PETMA	P33573 petromyzon
23	372.5	15.9	774	1 SCA_DROME	P21520 drosophila
24	190.5	8.1	129	1 MFA4_BOVIN	P55918 bos taurus
25	110	4.7	304	1 MMGL_MOUSE	P49300 mus musculus
26	110	4.7	876	1 MYSS_HUMAN	P12882 homo sapien
27	109.5	4.7	1940	1 MYSE_HUMAN	P11055 homo sapien
28	108	4.6	1805	1 HMW2_MYCGE	P47460 mycoplasma
29	106.5	4.6	1957	1 YD86_SCHPO	Q10411 schizosacch
30	106	4.5	1940	1 MYSE_RAT	P12847 rattus norv
31	105.5	4.5	692	1 MYS_PODCA	Q05000 podocoryne
32	105	4.5	872	1 TE95_TETTH	Q94819 tetrahymena
33	105	4.5	1102	1 MYSC_CHICK	P29616 gallus gall

34	104.5	4.5	455	1 VIME_CYPCA	Q92155 cyprinus ca
35	104.5	4.5	507	1 VLI_HPV37	P08133 human papil
36	104.5	4.5	1607	1 LMGI_MOUSE	P02468 mus musculu
37	104.5	4.5	1878	1 BRCL_CANFA	Q95153 canis famil
38	102.5	4.4	1300	1 DYNA_NEUCR	Q01397 neurospora
39	101.5	4.3	1940	1 MYSE_CHICK	P02565 gallus gall
40	101	4.3	1250	1 BXE_CLOBO	Q00496 clostridium
41	100.5	4.3	579	1 GI60_HUMAN	Q08378 homo sapien
42	100.5	4.3	950	1 Y136_HUMAN	Q14149 homo sapien
43	100.5	4.3	1107	1 VJEP_ECOLI	P39285 escherichia
44	100	4.3	450	1 VIMB_CARAU	P48673 carassius a
45	100	4.3	3433	1 UTRO_HUMAN	P46939 homo sapien

ALIGNMENTS

RESULT	1	
FIBX_MOUSE		
ID	FIBX_MOUSE	STANDARD; PRT; 432 AA.
AC	P12804:	
DT	01-OCT-1989 (Rel. 12, Created)	
DT	01-OCT-1989 (Rel. 12, Last sequence update)	
DE	PROTHROMBINASE PRECURSOR (FIBRINOGEN-LIKE PROTEIN) (CYTOTOXIC T-	
DE	LYMPHOCYTE SPECIFIC PROTEIN).	
GN	FIBLP OR FGL2.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=CYTOTOXIC T-CELL;	
RA	MEDLINE=87115521; Pubmed=3550794;	
RT	Koyama T., Hall L.R., Hasegawa W.G., Toneyaga S., Saito H.;	
RT	"Structure of a cytotoxic T-lymphocyte-specific gene shows a strong	
RT	homology to fibrinogen beta and gamma chains."	
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).	
RN	[2]	
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.	
RC	STRAIN=BALB/CJ; TISSUE=PERITONEAL MACROPHAGE;	
RX	MEDLINE=95333285; Pubmed=7609073;	
RA	Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,	
RA	Levy G.;	
RT	"Association of mouse fibrinogen-like protein with murine hepatitis.	
RT	virus-induced prothrombinase activity."	
RL	J. Virol. 69:5033-5038(1995).	
CC	-1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.	
CC	-1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC	
CC	T-CELLS.	
CC	-1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS	
CC	VIRUS STRAIN 3 (MHV-3).	
CC	-1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF	
CC	THE BETA AND GAMMA CHAINS OF FIBRINOGEN.	
CC	-----	
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CC	-----	
DR	EMBL; M16238; AAA37624.1;	
DR	EMBL; M15761; AAA37624.1; JOINED.	
DR	EMBL; S78773; AAB34823.1;	
DR	PIR; A27447; A27447.	
DR	HSSP; P02671; IFZD.	
DR	MGI; M103266; FGL2.	
DR	INTERPRO; IPR002181;	
DR	PFAM; PF00147; fibrinogen_C.1.	
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.	
KW	T-cell; Cytolysis; Blood coagulation; Signal.	

FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 PROTHROMBINASE.
FT DISULFID 206 235 BY SIMILARITY.
FT - DISULFID 364 377 BY SIMILARITY.
FT CONFLICT 332 332 A -> G (IN REF. 2).
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CCBA782 CRC64;

Query Match 100.0%; Score 2340; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGWLWLSAVLAACRAVEHNTEGLEDSAAQACPARLEGSGRCGSCPTQLTLP 60
Db 1 MRLPGWLWLSAVLAACRAVEHNTEGLEDSAAQACPARLEGSGRCGSCPTQLTLP 60
QY 61 TLTLPQLGSMMEVLEKVRLEKAVDSLKSCODCKLOADDDHDPGGNGGGAETAD 120
Db 61 TLTLPQLGSMMEVLEKVRLEKAVDSLKSCODCKLOADDDHDPGGNGGGAETAD 120
QY 121 SRVQELSSQVKNLSSELNKAQDOIGLQGRLETLHLVNMNNTIENYDNKVNLTVVVNSL 180
Db 121 SRVQELSSQVKNLSSELNKAQDOIGLQGRLETLHLVNMNNTIENYDNKVNLTVVVNSL 180
QY 181 DGKSCKCPSEHMQSQPVHLLYKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETM 240
Db 181 DGKSCKCPSEHMQSQPVHLLYKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETM 240
QY 241 GGGWTVLQARLDGSGNFTREWKDYKAGFNGLEFELWGNKDKTHLLTKSKEMILRIDLEDF 300
Db 241 GGGWTVLQARLDGSGNFTREWKDYKAGFNGLEFELWGNKDKTHLLTKSKEMILRIDLEDF 300
QY 301 NGLTYALYDQFYVANEFLKYRLHIGNYGTAGDALRFSRHHNHLRFTTTPDRNDRYP 360
Db 301 NGLTYALYDQFYVANEFLKYRLHIGNYGTAGDALRFSRHHNHLRFTTTPDRNDRYP 360
QY 361 SGNGLYSSGWFDSCLSANLNGYKHQYKGVNRGIFGWTPGINQAPGGYKSSFKO 420
Db 361 SGNGLYSSGWFDSCLSANLNGYKHQYKGVNRGIFGWTPGINQAPGGYKSSFKO 420
QY 421 AKMIRPKNFKP 432
Db 421 AKMIRPKNFKP 432

RESULT 2
FIBB_CHICK
ID FIBB_CHICK STANDARD; PRT: 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
cleavage site".
RL Biochemistry 30:3290-3294(1991).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC . POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC
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CC
CC EMBL; M58514; AAA48770.1; -
DR PIR; A38463; A38463.
DR HSP; P02675; LFZB.
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfatation.
FT PEPTIDE 1 17 FIBRINOPEPTIDE B.
FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
FT MOD_RES 5 5 SULFATATION (BY SIMILARITY).
FT SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
FT FIBRINOPEPTIDE B).
FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 397 410 BY SIMILARITY.
FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 21.1%; Score 493.5; DB 1; Length 463;
Best Local Similarity 30.4%; Pred. No. 8.2e-29;
Matches 137; Conservative 58; Mismatches 162; Indels 93; Gaps 14;

QY 30 EDASAAQACPARLEGSGRCE-----GSCQPFQLTLTFLTQLPRLGSMEEVLKEVRTL 83
Db 51 QDQAMKKGIPIYPDAGGCKHPIDELGVLCPTGCELOF-----TLKKQKTV 97
QY 84 KEAVDSLKSCQDKLQADDDHDPGGNGGGAETAEASRVQELSSQVKNLSSELNKAQD 143
Db 98 KPVLRDLK-----DRVAKFSD-----TSTMYQYVNMIDNKLKLVTKQKQKDN 139
QY 144 ---ILOGLRLETLHLVNMNNTIENYDNKVNLTVVVNSLDGKSCKCPSEHMQSQ----- 196
Db 140 DIILSEYNTMELHNYIKDNLNIPSSLRVLRRAVLDLSLHKIKLENAIATQDTCRS 199
QY 197 -----PVQHLIYKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQ 248
Db 200 PCVASCNIPV---VSGRECEDIYRKGGTSEMYIIQDPFTTPPYVYCDMETDNGGWTLIQ 257
QY 249 ARLDGSTNFTREWKDYKAGFNGLER-----EFWLGNDKIHLLTKSKEMILRIDL 297
Db 258 NRQDGSVNFGRAMDEYKRGFNIAKSGGKVKYCDPFGVWLGNDKISQLTKIGPTKVLIE 317
QY 298 EDNGLTYALYDQFYVANEFLKYRLHIGNYGTAGDALR--FSRHHN-----HDLRF 348
Db 318 EDWNGKVSALYGGFTTHNEGNYQLSVSNYKGNAGNALMEGASQLYQRTMTIHNGMY 377
QY 349 FTTPDRNDRY-----PSGNGLYSSGWFDSCLSANLNGYK-----HOKYKGVNRG 397
Db 378 FSTYDRNDGWLTFDPRKQCKSKEDGGGWWYNRCHAANPNRGYYWGWYSSWMAKHGTDG 437
QY 398 IFWGTWPGINQAPGGYKSSFKQAKMIRP 427

Db 438 IVMNWKG-----SWY--SKKMSMKIKP 459

RESULT 3

FIBG_HUMAN STANDARD; PRT; 437 AA.

AC P02679; FIBG_HUMAN

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FIBRINOGEN GAMMA-A CHAIN PRECURSOR.

GN FGG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85252774; PubMed=2990550;

RA Rixon M.W., Chung D.W., Davie E.W.;

RT "Nucleotide sequence of the gene for the gamma chain of human

RL fibrinogen.";

RL Biochemistry 24:2077-2086(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=83283434; PubMed=6688357;

RA Chung D.W., Chan W.-Y., Davie E.W.;

RT "Characterization of a complementary deoxyribonucleic acid coding for

RL the gamma chain of human fibrinogen.";

RL Biochemistry 22:3250-3256(1983).

RN [3]

RP SEQUENCE OF 27-437.

RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;

RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some

RL structural variants.";

RL (In) Peeters H. (eds.);

RL Pergamon Press, Oxford (1980).

RN [4]

RP SEQUENCE OF 75-286 FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=92119334; PubMed=1685103;

RA Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.;

RT "Polymorphism of the human gamma chain fibrinogen gene.";

RL DNA Seq. 1:419-422(1991).

RN [5]

RP SEQUENCE OF 285-437 FROM N.A.

RX MEDLINE=85030379; PubMed=6092346;

RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,

RA Crabtree G.R.;

RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA

RL splicing near the 3' end of the gene produces gamma A and gamma B

RL forms of gamma-fibrinogen.";

RL J. Biol. Chem. 259:12826-12830(1984).

RN [6]

RP SEQUENCE OF 209-270 FROM N.A.

RX MEDLINE=84069777; PubMed=6689067;

RA Inam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;

RT "Isolation and characterisation of cDNA clones for the A alpha- and

RL gamma-chains of human fibrinogen.";

RL Nucleic Acids Res. 11:7427-7434(1983).

RN [7]

RP REVIEW, AND DISULFIDE BONDS

RX MEDLINE=83254370; PubMed=6575689;

RA Henschen A., Lottspeich F., Kehl M., Southan C.;

RT "Covalent structure of fibrinogen.";

RL Ann. N.Y. Acad. Sci. 408:28-43(1983).

RN [8]

RP DISULFIDE BONDS.

RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,

RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;

RT "The structures of fibrinogen and fibrin.";

RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,

RL Neurath H. (eds.);

RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).

RN [9]

RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,

RL Pergamon Press, New York (1978).

RN [9]

RP DISULFIDE BONDS.

RX MEDLINE=76225080; PubMed=936108;

RA Blombaeck B., Hessel B., Hogg D.;

RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";

RL Thromb. Res. 8:639-658(1976).

RN [10]

RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.

RX MEDLINE=83231465; PubMed=6860649;

RA Hoeprich P.D., Doolittle R.F.;

RT "Dimeric half-molecules of human fibrinogen are joined through

RL disulfide bonds in an antiparallel orientation.";

RL Biochemistry 22:2049-2055(1983).

RN [11]

RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE=84305751; PubMed=6383194;

RA Doolittle R.F.;

RT "Fibrinogen and fibrin.";

RL Annu. Rev. Biochem. 53:195-229(1984).

RN [12]

RP POLYMERIZATION SITE.

RX MEDLINE=85014892; PubMed=6592597;

RA Horwitz B.H., Varadi A., Scheraga H.A.;

RT "Localization of a fibrin gamma-chain polymerization site within

RL segment Thr-374 to Glu-396 of human fibrinogen.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).

RN [13]

RP POLYMERIZATION SITE.

RX MEDLINE=81142375; PubMed=6451630;

RA Oleksa S.A., Budzynski A.Z.;

RT "Localization of a fibrin polymerization site.";

RL J. Biol. Chem. 256:3544-3549(1981).

RN [14]

RP PLATELET AGGREGATION SITE.

RX MEDLINE=84203545; PubMed=6326808;

RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;

RT "Platelet receptor recognition site on human fibrinogen. Synthesis

RL and structure-function relationship of peptides corresponding to the

RL carboxy-terminal segment of the gamma chain.";

RL Biochemistry 23:1767-1774(1984).

RN [15]

RP PLATELET AGGREGATION SITE.

RX MEDLINE=84185664; PubMed=6325435;

RA Plow E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.;

RT "Evidence that three adhesive proteins interact with a common

RL recognition site on activated platelets.";

RL J. Biol. Chem. 259:5388-5391(1984).

RN [16]

RP CALCIUM-BINDING SITE.

RX MEDLINE=85261382; PubMed=3160702;

RA Dang C.V., Ebert R.F., Bell W.R.;

RT "Localization of a fibrinogen calcium binding site between

RL gamma-subunit positions 311 and 336 by terbium fluorescence.";

RL J. Biol. Chem. 260:9713-9719(1985).

RN [17]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.

RX MEDLINE=97169449; PubMed=9016719;

RA Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W.,

RA Davie E.W., Stenkamp R.E., Teller D.C.;

RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma

RL chain of human fibrinogen.";

RL Structure 5:125-138(1997).

RN [18]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.

RX MEDLINE=97352771; PubMed=9207064;

RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;

RT "The primary fibrin polymerization pocket: three-dimensional

RL structure of a 30-kDa C-terminal gamma chain fragment complexed with

RL the peptide Gly-Pro-Arg-Pro.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).

RN [19]

```

145 --QKIVLNKEVAQLEAQCE--PKDVTQV---IHDTGKDCQDIANKAKQSGLYFIKP 197
225 DHRNSSFEVYCDMETGGGWTYVLAERLDGSGTFTREWKDYKAGFCNLE----REFWLGND 280
198 LKANQOPLVYCEIDGSGNGWTVPQKRLDGSVDFFKKNWIOYKEGFGHLSPTGTTFEVLGNE 257
281 KIHLLTKSKEM--ILRLIDLEDFNGLTYALYDQFVYVANEFLKYRLHIGNY-NGTAGDAL- 336
258 KIHLLISTQSAIPALRVLELDNWRSTADYAMFKVGPEDAKYRLTYAYFAGGDGDAFD 317
337 -----RFSRHYNHDLRFETTPDRDNDRYPSGNCGLYYSGWGFDSCLSANLNGKY 386
318 GFDFGDDPSDKF--FTSHNGMOPSTWDNDNDRKF-EGNCAEQDGSQWMMKNKCHAGHLNGVY 374
387 YH-----QKYKGVNRGIFGWTPGNGINQAOPGGYKS---SPKQAKMIRPN 429
375 YQGGTYSKASTPNGYDNGIATW-----KTRWYSMKKTTMKIIPFN 416

RESULT_4
FIBH_HUMAN
ID FIBH_HUMAN STANDARD; PRT; 453 AA.
AC P04469; P04470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA').
GN FGG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85252774; PubMed=2990550;
RA Rixon M.W., Chung D.W., Davie E.W.;
RT "Nucleotide sequence of the gene for the gamma chain of human
RL fibrinogen.";
RT Biochemistry 24:2077-2086(1985).
RN [2]
CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
RX MEDLINE=81054908; PubMed=6933547;
RA Wolfenstein-Todel C., Mosesson M.W.;
RT "Human plasma fibrinogen heterogeneity: evidence for an extended
RL carboxyl-terminal sequence in a normal gamma chain variant
RT (gamma').";
RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
RN [3]
SEQUENCE OF 285-453 FROM N.A.
RX MEDLINE=85030379; PubMed=6092346;
RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
RA Crabtree G.R.;
RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
RT splicing near the 3' end of the gene produces gamma A and gamma B
RL forms of gamma-fibrinogen.";
RL J. Biol. Chem. 259:12826-12830(1984).
RN [4]
SEQUENCE OF 411-453.
RX MEDLINE=82068993; PubMed=7306501;
RA Wolfenstein-Todel C., Mosesson M.W.;
RT "Carboxy-terminal amino acid sequence of a human fibrinogen
RL gamma-chain variant (gamma').";
RL Biochemistry 20:6146-6149(1981).
RN [5]
SULFATATION.
RX MEDLINE=91369960; PubMed=1892842;
RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
RT "Recombinant human fibrinogen and sulfation of the gamma' chain.";
RL Biochemistry 30:9414-9420(1991).
CC !- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC !- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

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Db	56	CPKRISHSPEYP-----RDCYD--ILQSCGSGSPSPGGYYIQPDGGN-LIKVYCDMETD	10
Qy	241	GGGTVTLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMILRIDLEDF	300
Db	107	EGGTVFQRRIDGTINFYRSWSYYQTGFGMLNTEFWLGNDNIHYLLSQGDYELRVELNNT	166
Qy	301	NGLTLYALYDQFYVYANEFKLRLHIGNYNTAGDALRFSRHYNHLRFFTTDPDNDNDYRP	360
Db	167	LGNHYAYAKNKRIGDGSFSEVLLVIGAYSCTAGDSLAY-----HNTMRSTVDNDNDVY-	220
Qy	361	SGNCGLYSSG---WWFDSCLSANLCKYHYHQYKGVNRGIFGWTPGGINQAOPGGYKSS	417
Db	221	SINCASHSSYGRGAWWYKSCLLSNLNGQY--DYSGAPS-IYWSYLPDGDNDQIP-----	271
Qy	418	FKOAKMMIR 426	
Db	272	FAEMKLRNR 280	
RESULT	8		
FIBB_HUMAN			
ID	FIBB_HUMAN	STANDARD;	PRT; 491 AA.
AC	P02675;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	FIBRINOGEN BETA CHAIN PRECURSOR.		
GN	FGB.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91344740; PubMed=2102623;		
RA	Chung D.W., Harris J.E., Davie E.W.;		
RT	"Nucleotide sequences of the three genes coding for human		
RT	fibrinogen.";		
RL	Adv. Exp. Med. Biol. 281:39-48(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=83283433; PubMed=6688356;		
RA	Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;		
RT	"Characterization of complementary deoxyribonucleic acid and genomic		
RT	deoxyribonucleic acid for the beta chain of human fibrinogen.";		
RL	Biochemistry 22:3244-3250(1983).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RL	Chung D.W., Harris J.E., Davie E.W.;		
RL	(In) Chien S. (eds.);		
RL	Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,		
RL	Plenum Press, New York (1991).		
RN	[4]		
RP	SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.		
RA	Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;		
RT	"Human fibrinogen: sequence, sulfur bridges, glycosylation and some		
RT	structural variants.";		
RL	(In) Peeters H. (eds.);		
RL	Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,		
RL	Pergamon Press, Oxford (1980).		
RN	[5]		
RP	SEQUENCE OF 31-491.		
RA	MEDLINE=79124640; PubMed=420779;		
RX	Watt K.W.K., Takagi T., Doolittle R.F.;		
RT	"Amino acid sequence of the beta chain of human fibrinogen.";		
RL	Biochemistry 18:68-76(1979).		
RN	[6]		
RP	SEQUENCE OF 31-148, AND DISULFIDE BONDS.		
RA	MEDLINE=76225080; PubMed=936108;		
RA	Blomback B., Hessel B., Hogg D.;		
RT	"Disulfide bridges in NH2-terminal part of human fibrinogen.";		
RT	Thromb. Res. 8:639-658(1976).		
RN	[7]		
RP	SEQUENCE OF 1-38 FROM N.A.		

RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RT beta gene.";
 RN Nucleic Acids Res. 15:1615-1625(1987).
 RN [8]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RN Acta Chem. Scand. 19:1788-1789(1965).
 RN [9]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschel A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RN Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [10]
 RP DISULFIDE BONDS
 RX MEDLINE=77245999; PubMed=891553;
 RA Gardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RT disulfide-containing cyanogen-bromide fragments.";
 RN Eur. J. Biochem. 77:595-610(1977).
 RN [11]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RN (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [12]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RN Annu. Rev. Biochem. 53:195-229(1984).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=933233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RN Nature 389:455-462(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292393; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RN Biochemistry 37:8637-8642(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RN Biochemistry 38:2941-2946(1999).
 RN [16]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE=89058942; PubMed=3194892;
 RA Schmelzer C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RT structural studies of fibrinogen Baltimore II.";
 RN Thromb. Res. 52:173-177(1988).
 RN [17]
 RP VARIANT ISE.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the

RT replacement of B beta glycine-15 by cysteine.";
 RN Blood 77:1958-1963(1991).
 RN [18]
 RP VARIANT NAPLES.
 RX MEDLINE=92340564; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta
 RT 68 Ala-->Thr.";
 RN J. Clin. Invest. 90:238-244(1992).
 RN [19]
 RP VARIANTS LJMUIDEN AND NIJMEGEN
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens IJmuiden (B beta Arg14-->Cys) and Nijmegen (B
 RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [20]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene.";
 RN J. Biol. Chem. 260:4390-4396(1985).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -!- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; J00129; AAA52429.1; -
 CC EMBL; J00131; AAA98115.1; -
 CC EMBL; J00130; AAA98115.1; JOINED.
 CC EMBL; J00132; AAA98116.1; -
 CC EMBL; J00133; -; NOT_ANNOTATED_CDS.
 CC EMBL; X05018; CAA28674.1; -
 CC EMBL; M64983; AAA18024.2; -
 CC EMBL; M26877; AAA52445.1; -
 CC EMBL; M26876; AAA52445.1; JOINED.
 CC PIR; B43568; FCHUB.
 CC PDB; 1FZA; 03-DEC-97.
 CC PDB; 1FZB; 03-DEC-97.
 CC PDB; 1FZC; 14-OCT-98.
 CC PDB; 1FZE; 08-JUN-99.
 CC PDB; 1FZF; 08-JUN-99.
 CC PDB; 1FZG; 08-JUN-99.
 CC SWISS-2DPAGE; P02675; HUMAN.
 CC MIM; 134830; -

QY 268 FGNLER-----EFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVA 315
 DB 280 FGNATNAEGKKYCGVPGCEYWGNDRIQSOLNMGFTKLLIEMENKGDVKTALYEGFTVQ 339
 QY 316 NEFLKYLRLHIGNYGTAGDAL-----RFSRHYNHDLRFTTPDRDNDRY-----PSG 362
 DB 340 NEANKYQLSVSKYGTAGNALIEGASQVNGENTWTFINSMEFFSYDRDNDGKWTDPK 399
 QY 363 NCGLYYSSGWWFDCSLSANLKKYY-----HOKYKGVNRGIFGWTWPGINOAOPGGYK 415
 DB 400 QCSKEDGGGWWYRCHAAANPNRGYWGCAWTYDMAKHGTDDGVVMMNMQ-----SWT- 452
 QY 416 SSFQOAKMIRP 427
 DB 453 -SMKKMSMKIRP 463

RESULT 10
 FIBA_HUMAN
 ID FIBA_HUMAN STANDARD; PRT; 866 AA.
 AC P02671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
 GN FGA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RX SEQUENCE FROM N.A. (ALPHA-E FORM).
 RX MEDLINE=93090725; PubMed=1457396;
 RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
 RA Roy S.N., Redman C.M., Griening G.;
 RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
 RT subunit: a novel exon conferring marked homology to beta and gamma
 RT subunits.";
 RL Biochemistry 31:11968-11972(1992).
 RN [2]
 RX SEQUENCE FROM N.A. (ALPHA-E FORM).
 RA Chung D.W., Griening G.;
 RL (In) Ebert R.F. (eds.);
 RL Index of variant human fibrinogens, pp.13-24, CRC Press,
 RL Boca Raton (1994).
 RN [3]
 RX SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
 RC TISSUE=LIVER;
 RX MEDLINE=91344740; PubMed=2102623;
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RT fibrinogen.";
 RL Adv. Exp. Med. Biol. 281:39-48(1990).
 RN [4]
 RX SEQUENCE FROM N.A. (ALPHA FORM).
 RX MEDLINE=83247396; PubMed=6575389;
 RA Kant J.A., Lord S.T., Crabtree G.R.;
 RT "Partial mRNA sequences for human A alpha, B beta, and gamma
 RT fibrinogen chains: evolutionary and functional implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
 RN [5]
 RX SEQUENCE OF 1-629 FROM N.A.
 RX MEDLINE=83283432; PubMed=6688355;
 RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT the alpha chain of human fibrinogen.";
 RL Biochemistry 22:3237-3244(1983).
 RN [6]
 RX SEQUENCE OF 20-629.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,

RL Pergamon Press, Oxford (1980).
 RN [7]
 RX SEQUENCE OF 20-629, AND DISULFIDE BONDS.
 RX MEDLINE=80088231; PubMed=518846;
 RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 RT Overlapping sequences providing the complete sequence.";
 RL Biochemistry 18:5410-5416(1979).
 RN [8]
 RX SEQUENCE OF 110-156 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Inam A.M., Eaton M.A., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [9]
 RX SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
 RX MEDLINE=83254384; PubMed=6575700;
 RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
 RT "Cloning of fibrinogen genes and their cDNA.";
 RL Ann. N.Y. Acad. Sci. 408:449-456(1983).
 RN [10]
 RX SEQUENCE OF 20-35.
 RP Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [11]
 RX CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=80088230; PubMed=518845;
 RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 RT Exact location of cross-linking acceptor sites.";
 RL Biochemistry 18:5405-5410(1979).
 RN [12]
 RX CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=78130085; PubMed=632262;
 RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
 RT "Localization of the alpha-chain cross-link acceptor sites of human
 RT fibrin.";
 RL J. Biol. Chem. 253:2184-2195(1978).
 RN [13]
 RX VARIANT, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [15]
 RX CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
 RX MEDLINE=87057190; PubMed=2877981;
 RA Kimura S., Aoki N.;
 RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
 RL J. Biol. Chem. 261:15591-15595(1986).
 RN [16]
 RX PHOSPHORYLATION.
 RX MEDLINE=84104274; PubMed=6318767;
 RA Itarte E., Plana M., Guasch M.D., Martos C.;
 RT "Phosphorylation of fibrinogen by casein kinase 1.";
 RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
 RN [17]
 RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
 RX MEDLINE=92218459; PubMed=1560020;
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RT "The structure of residues 7-16 of the A alpha-chain of human
 RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920(1992).
 RN [18]
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.

RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RL crosslinked counterpart from fibrin.";
RN Nature 389:455-462(1997).
[19]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX MEDLINE=982923395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RL different bound ligands.";
RN Biochemistry 37:8637-8642(1998).
[20]
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX MEDLINE=98356117; PubMed=9689040;
RA Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RA Redman C., Doolittle R.F., Grieninger G.;
RT "Crystal structure of a recombinant alphaEC domain from human
RL fibrinogen-420.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
[21]
RX X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RN Biochemistry 38:2941-2946(1999).
[22]
RX VARIANT KYOTO-2.
RX MEDLINE=91300048; PubMed=20700049;
RA Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
RL characterized by the replacement of A alpha proline-18 by leucine.";
RN Blood 78:149-153(1991).
[23]
RX VARIANT LIMA.
RX MEDLINE=92340680; PubMed=1634621;
RA Takahashi N., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA Perez-Requejo J.L., Matsuda M.;
RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A
RL alpha-arginine-141 to serine substitution associated with extra
RN N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
formation but normal fibrin-facilitated plasminogen activation
catalyzed by tissue-type plasminogen activator.";
RN J. Clin. Invest. 90:67-76(1992).
[24]
RX VARIANT CARACAS-2.
RX MEDLINE=91268018; PubMed=1675636;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA Arocha-Pinango C.L., Matsuda M.;
RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RL dysfibrinogen, fibrinogen Caracas II, characterized by impaired
RN fibrin gel formation.";
RN J. Biol. Chem. 266:11575-11581(1991).
[25]
RX VARIANT DUSART.
RX MEDLINE=93232289; PubMed=8473507;
RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
RA Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA Caen J.P.;
RT "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
RL its association with abnormal fibrin polymerization and
RN thrombophilia.";
RN J. Clin. Invest. 91:1637-1643(1993).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC DIVERGING FROM THIS NODE ARE 2 THREE-CHAIN COILED COILS, WHICH
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODE.
CC DIVERGING FROM THIS NODE ARE 2 THREE-CHAIN COILED COILS, WHICH

Query Match 19.4%; Score 454; DB 1; Length 866;
Best Local Similarity 39.4%; Pred. No. 1.4e-25;
Matches 102; Conservative 41; Mismatches 74; Indels 42; Gaps 11;
QY 192 HMQSQPVQHLIYKDCSDHYVL-----GRRSSGAYRVPDPHNSSEFFVYCDMETMGGGTVL 247
DB 623 HAKSRPV-----RDCDD--VLQTHPSGTQSGIFNKLPGSSKIFSYCDQETSLSGWLII 675
QY 248 QARLDGSTNFTREWDYKAGFNL-----BREFWLGNDKIHLTKSKEMILRIDLEDFNGL 303
DB 676 QORMDGLSNFTWQDYKRGFGSLNDEGGEGFWLGNLYLHLTQ-RGSLVRLVELEDAWN 734
QY 304 TLYALYDQFYVANEFKLYRLHICNGYTAGDAL-----RFSRHYNHLRFFFTTPORDND 357
DB 735 EAYAEV-HFRVSGEAGYALQVSSYEGTAGDALIEGSVEEGAETTSNNMQSFORDAD 793
QY 358 RYPSNCGLYSYSSGWFDSCLSANLKKY-----HOKYKGVNRNGIFNGTWPQINO 408
DB 794 QWEE-NCAEVYGGWYNNCQANLNGIYPPGSGYDPRNNSPYE-TENGWVWVSFRGADY 851
QY 409 AQPGCYKSFQAKMIRP 427
DB 852 -----SLRAVRMKIRP 862
RESULT 11
FIBA_RAT STANDARD; PRT; 782 AA.
ID FIBA_RAT
AC P06399;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA Fu Y., Cao Y., Hertzberg K., Grieninger G.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ALPHA FORM).
RX MEDLINE=86011580; PubMed=4046033;
RA Crabtree G.R., Comeau C.M., Fowkes D.M., Fornace A.J. Jr.,
RA Malley J.D., Kant J.A.;
RT "Evolution and structure of the fibrinogen genes. Random insertion of
RL introns or selective loss?";
RN J. Mol. Biol. 185:1-19(1985).
[3]
RP SEQUENCE OF 20-36.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
[4]
RP SEQUENCE OF 458-550 FROM N.A. (ALPHA FORM).
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=87134033; PubMed=3817019;
RA Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
RL liver regeneration.";
RN Exp. Cell Res. 169:47-56(1987).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC DIVERGING FROM THIS NODE ARE 2 THREE-CHAIN COILED COILS, WHICH
CC CONNECT THE CENTRAL NODE TO THE DISTAL NODES CONTAINING THE
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.

Query Match 19.08; Score 444; DB 1; Length 479;
Best Local Similarity 32.6%; Pred. No. 3.5e-25;
Matches 116; Conservative 48; Mismatches 118; Indels 74; Gaps 11;

QY 119 EDSRVOELESQVNLSSLLKNAKQIQLOGLEFLHLVNMNNIENYVDNKVANLTV--- 175
DB 146 KQAVQKQNVINVEYSSILEDKLYID-----EFVN-----DNIPNLRLVLR 188
QY 176 VNSLDGKCKSCPSQEHMQSQ-----PVHLLYKDCSDHYVLGRSSGAYRYT 223
DB 189 ILEDLRKMQKLEDISAQTEYCHTPCTVNCNIPV--VSGKECEHILKRGSTSEMYLIQ 246
QY 224 PDHRNSSFEVYCDMETMGWGTVQLARLDGSTNFTREWKDYKAGFGN-----L 271
DB 247 PDTSSKPYRYCDMKTENGWGTVIQNRQDGSVDFGRKKWDPYKKGFGNIATNEDTKKYCGL 306
QY 272 EREWLGNDRKTHLLTKSEMILRDLDFNGLTYALYDQFVYANEFLLKRLHIGNYGT 331
DB 307 PGEYWLGNDRKISQLTRIGPTTELLIEMDWKGDVKARHYGGFTVQTEANKYQVSVNRYKGT 366
QY 332 AGDALRFSRHY-----NHDLRFFFTPDNDRY-----PSGNCGLYVSSGWFDFDSC 378
DB 367 AGNALMEGASQALVGENRTMTTHNGFFSTYDRDNDGWVTTDPRKQCKSDGGGWNINRCH 426
QY 379 SANLNGKYY-----HOKYKGVNRGIFWGTWPGINQAPGGYKSFQKQAKMIRP 427
DB 427 AANPNRYWGGLYSWDSKDKTGDGVVMMNKG-----SWY--SMRRSMKIRP 474

RESULT 14
FIBG RAT STANDARD; PRT; 445 AA.
AC P02680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FIBRINOGEN GAMMA-A/-B CHAIN PRECURSOR.
GN FGG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129318; PubMed=6897622;
RA Crabtree G.R., Kant J.A.;
RT "organization of the rat gamma-fibrinogen gene: alternative mRNA
RT splice patterns produce the gamma A and gamma B (gamma ') chains of
RT fibrinogen.";
RL Cell 31:159-166(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87174801; PubMed=3562236;
RA Morgan J.G., Holbrook N.J., Crabtree G.R.;
RT "Nucleotide sequence of the gamma chain gene of rat fibrinogen:
RT conserved intronic sequences.";
RL Nucleic Acids Res. 15:2774-2776(1987).
RN [3]
RP SEQUENCE OF 1-102 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- ALTERNATIVE PRODUCTS: GAMMA-B IS FORMED FROM THE SAME GENE AS
CC GAMMA-A, PROBABLY AS A RESULT OF FAILURE TO SPICE OUT THE LAST
CC INTRON DURING MRNA PROCESSING.

-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
MONOMERS.

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EMBL; J00733; ; NOT ANNOTATED_CDS.
EMBL; J00734; ; NOT ANNOTATED_CDS.
EMBL; J00735; ; NOT ANNOTATED_CDS.
EMBL; X05860; CAA29289.1; .
EMBL; X05861; CAA29289.1; JOINED.
EMBL; A01337; AAA98626.1; .
PIR; A01327; FERTCA.
PIR; A03128; FERTGB.
DR HSSP; P02679; LFID.
DR INTERPRO; IPR002181; .
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma;
KW Alternative splicing; Signal.
FT SIGNAL 1 25
FT CHAIN 26 445 FIBRINOGEN GAMMA-B CHAIN.
FT DISULFID 34 34 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 35 35 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 45 45 INTERCHAIN (WITH THE BETA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 49 49 INTERCHAIN (WITH THE ALPHA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 161 161 INTERCHAIN (WITH THE BETA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 165 165 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 179 208 (BY SIMILARITY).
FT DISULFID 352 365 (BY SIMILARITY).
FT DISULFID 435 437 SVE -> GDM (IN GAMMA-A CHAIN).
FT VARSPLIC 438 445 MISSING (IN GAMMA-A CHAIN).
FT CONFLICT 296 296 E -> G (IN CDNA).
SQ SEQUENCE 445 AA; 50632 MW; 9D61CCC0168B17A9 CRC64;

Query Match 18.6%; Score 435; DB 1; Length 445;
Best Local Similarity 31.1%; Pred. No. 1.4e-24;
Matches 118; Conservative 51; Mismatches 130; Indels 80; Gaps 14;

QY 113 NGAEATDSRVOELESQVNLSSLLKNAKQIQLOG----- 149
DB 56 NSYQTDVDTDLQTLLENILQRAENRTTEAKELIKAIQVYVNPDPKPKMIEGATQSKKM 115
QY 150 -----RLETLHLVNMNNI-----ENVYDN--KVALNTVVNSLDGKCKSCPSQEHMQSQPV 198
DB 116 VEELKYEALLTHESIRVLDIYTSNKKQITNLKQVQALCOE-PCKDSVR---I 171
QY 199 QHLLYKDCSDHYVLGRSSGAYRYTPDHRNSSFEVYCDMETMGWGTVQLARLDGSTNFT 258
DB 172 YDITGKQCDQTANKGAKESGLYSIRPLKATEQFLVYCTDGPNGWTEFKRLDGSVDLF 231
QY 259 REWKDYKAGFGNLE-----REFWLGNDRKTHLLTKSEM--ILRIDLEDFNGLTYALYDQF 312
DB 232 KNWIOYKEGFGHLSPTGTTTEFWLGNDRKTHLLTKSEM--ILRIDLEDFNGLTYALYDQF 291

QY 313 YVANEFLKYLHLGNY-NGTAGDAL-----RFSRHYNDLRFRTTPDRDNDRYP 360
Db 292 RVGPESDKYRLTYAYFTGGADGAFDGYDFGDDPSDF--FTSHGMHFSTWDNDKX- 348
QY 361 SGNCGLYSSGWFSDCLSANLNGKYH-----QYKGYVRNCFWGTWPGINOAQPGG 413
Db 349 EGNCAEQDGSWMWKNKCHAGLNGVYIOGGTYSKSTPNGYDNGIWIATW----- 398
QY 414 YKS---SFKQAKMIRPKN 429
Db 399 -KTRWYSMKETTKIIPFN 416
RESULT 15
FIBA_CHICK STANDARD; PRT; 741 AA.
AC P14448;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE OF 1-4 FROM N.A.
RA Greninger G.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-741 FROM N.A.
RX MEDLINE=90311369; PubMed=2367530;
RA Weissbach L., Grieneringer G.;
RT "Bipartite mRNA for chicken alpha-fibrinogen potentially encodes an
RT amino acid sequence homologous to beta- and gamma-fibrinogens.";
RL proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
RN [3]
RP SEQUENCE OF 19-33.
RX MEDLINE=78187470; PubMed=656462;
RA Takagi T., Finlayson J.S., Iwanaga S.;
RT "Amino acid sequence of chicken fibrinopeptide A.";
RL Biochim. Biophys. Acta 534:161-164(1978).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
CC PREDOMINANT FORM.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20803; AAB60686.1; JOINED.
DR EMBL; U20799; AAB60686.1; JOINED.
DR EMBL; U20800; AAB60686.1; JOINED.
DR EMBL; U20801; AAB60686.1; JOINED.
DR EMBL; U20802; AAB60686.1; JOINED.
DR EMBL; U20803; AAB60686.1; JOINED.
DR EMBL; U20799; AAB60685.1; JOINED.
DR EMBL; U20800; AAB60685.1; JOINED.
DR EMBL; U20801; AAB60685.1; JOINED.

DR EMBL; U20802; AAB60685.1; JOINED.
DR EMBL; M34096; AAA99306.1; -.
DR EMBL; M34096; AAA99307.1; -.
DR HSSP: P02671; 1FZD.
DR INTERPRO: IPR002181; -.
DR PFAM: PF00147; fibrinogen_C; 1.
KW PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Signal; Alternative splicing.
FT SIGNAL 1 18
FT PEPTIDE 19 33 FIBRINOPEPTIDE A.
FT CHAIN 34 741 FIBRINOGEN ALPHA-E CHAIN.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 46 46 INTERCHAIN (WITH C-42') (BY SIMILARITY).
FT DISULFID 55 55 INTERCHAIN (WITH THE BETA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 64 64 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 68 68 INTERCHAIN (WITH THE BETA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 180 180 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 184 184 INTERCHAIN (WITH THE BETA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 310 341 BY SIMILARITY.
FT SITE 33 34 CLEAVAGE (BY THROMBIN; RELEASE
FT VARSPLIC 506 509 FIBRINOPEPTIDE A).
FT VARSPLIC 510 741 DCDD -> GTQK (IN ISOFORM ALPHA).
FT MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE 741 AA; 82438 MW; A09F5F4F186DE3A6 CRC64;
Query Match 18.4%; Score 431.5; DB 1; Length 741;
Best Local Similarity 39.2%; Pred. No. 5.1e-24;
Matches 96; Conservative 39; Mismatches 77; Indels 33; Gaps 11;
Qy 204 KDCSD---HYVLGRSSGAYRVPDHRNSFEVYCDMETMGGGVTVLQARLDGSGNFTRE 260
Db 505 KDCDDIRQKHTSGAK-SGIFKIKPEGSNKVLSVYCDQETTLGGWLLIQORMDGSVNFRT 563
Qy 261 WKDYKAGFGNL-----EREFWLGNDKIHLTKSKEMILRIDLEDFNLGLTYALYDQFYVAN 316
Db 564 WQYRRGFGSDVKGQGGELWLGNIHLITQN-DTLRLVELEDWDGNAAYAEY-IVQVGT 621
Qy 317 EFLKYLHLGNYNGTAGDAL-----RFSRHYNDLRFRTTPDRDNDRYPGNCGLYSS 370
Db 622 EAEGTALTVSSTEGTAGDALVAGWLEGESEYTSQAQMDFSTFDRDDHWEE-SCAEVYGG 680
Qy 371 GWFVDSCLSANLNGKY-----YHOKYK---GVRNGIFWGTWPGINOAQPGGYSFKQAK 422
Db 681 GWYNSCOAANLGIYYPGGHYDPRYNNPYEENGWVWLPF-----RASDY--SLKVVR 732
Qy 423 WMIRP 427
Db 733 MKIRP 737

Search completed: February 27, 2001, 12:52:04
Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:50:10 ; Search time 31.84 Seconds
(without alignments)
921.265 Million cell updates/sec

Title: US-09-442-143-4
Perfect score: 2340
Sequence: 1 MRLPGWLSSAVLAACRAV.....GYKSFQKQMMIRPKNEKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2340	100.0	432	2 A27447	cytotoxic T-lympho
2	2336	99.8	432	2 I56934	fibrinogen-like pr
3	1853.5	79.2	439	2 I37391	fibrinogen-like pr
4	519.5	22.2	312	2 JN0596	fibrinogen-related
5	493.5	21.1	463	2 A38463	fibrinogen beta ch
6	489.5	20.9	437	1 FGHUG	fibrinogen gamma-A
7	489.5	20.9	453	1 FGHUGB	fibrinogen gamma-B
8	470.5	20.1	479	2 A25052	fibrinogen beta ch
9	466	19.9	444	2 S05313	fibrinogen gamma-B
10	463.5	19.8	282	2 A35084	fibrinogen-related
11	463	19.8	334	2 JC5980	ficolin-A precursor
12	463	19.8	491	1 FGHUB	fibrinogen beta ch
13	458	19.6	468	1 FGHUB	fibrinogen beta ch
14	454.5	19.4	1353	1 JH0675	restrictin precurs
15	454	19.4	866	2 D44234	fibrinogen alpha c
16	448.5	19.2	438	2 A32670	fibrinogen gamma c
17	446.5	19.1	1356	2 A45445	janusin precursor,
18	436	18.6	326	2 B47172	ficolin-beta - pig
19	435	18.6	323	2 A47172	transforming growt
20	435	18.6	326	2 S61517	ficolin-1 precursor
21	426.5	18.2	432	1 FGLMGS	fibrinogen gamma c
22	420	17.9	328	2 A05299	fibrinogen beta ch
23	420	17.9	437	1 FGTGA	fibrinogen gamma-A
24	420	17.9	445	1 FGTGB	fibrinogen gamma-B
25	416.5	17.8	1810	1 A32230	tenascin precursor
26	414.5	17.7	3566	1 A40701	tenascin-X precurs
27	412.5	17.6	220	2 S28170	tenascin homolog -
28	412.5	17.6	417	2 S65944	tenascin-X - pig (
29	412.5	17.6	4135	2 T42629	tenascin-X - bovin

30	409	17.5	2019	1 J01322	tenascin precursor
31	408.5	17.5	1746	1 S19694	tenascin precursor
32	406.5	17.4	2201	1 A32160	tenascin-C - human
33	402.5	17.2	860	2 I48839	tenascin-X - mouse
34	402.5	17.2	4006	2 T09070	probable tenascin
35	395.5	16.9	1914	2 T42635	tenascin y precurs
36	374	16.0	641	1 A41932	fibrinogen alpha-I
37	372.5	15.9	774	2 A39832	scarbous locus (sc
38	372.5	15.9	774	2 S58998	scarbous protein p
39	224.5	9.6	463	2 T15876	hypothetical prote
40	200.5	8.6	915	2 T21773	hypothetical prote
41	200.5	8.6	927	2 T21772	hypothetical prote
42	189.5	8.1	127	2 PC2036	microfibril-associ
43	170	7.3	431	2 T29850	hypothetical prote
44	169	7.2	452	2 T26827	hypothetical prote
45	165.5	7.1	146	2 T32255	hypothetical prote

ALIGNMENTS

RESULT 1

A27447

cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447

R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987

A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology
A:Reference number: A27447; MUID:87175527

A:Accession: A27447

A:Molecule type: mRNA

A:Residues: 1-432 <KOY>

A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <PBG>

Query Match 100.0%; Score 2340; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.7e-159;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRLPGWLSSAVLAACRAVEHNLTGLEDASAQAACPARLEGSGRCGSCPQLTLP	60
Db	1	MRLPGWLSSAVLAACRAVEHNLTGLEDASAQAACPARLEGSGRCGSCPQLTLP	60
Qy	61	TLFTQLPQLGSMEEVLKEVRTLKEAVDSLKKSCODCKLOADDHRDPGNGGNGAETAE	120
Db	61	TLFTQLPQLGSMEEVLKEVRTLKEAVDSLKKSCODCKLOADDHRDPGNGGNGAETAE	120
Qy	121	SRVQELSSQVANKLSSELNAKDQIQGLQRLTFLHVNMMNIENYVNDKVANLTVVVNSL	180
Db	121	SRVQELSSQVANKLSSELNAKDQIQGLQRLTFLHVNMMNIENYVNDKVANLTVVVNSL	180
Qy	181	DKGSKCPQSEHMQSPVQHLYIKDCSDHYVLGRSSGAYRVTDPHRNSSFEVYCDMETM	240
Db	181	DKGSKCPQSEHMQSPVQHLYIKDCSDHYVLGRSSGAYRVTDPHRNSSFEVYCDMETM	240
Qy	241	GGGWTVLQARLDGSGTNTREWKDYKAGFNLEREPWLNKDKTHLLTKSKEMTLRLDLEDF	300
Db	241	GGGWTVLQARLDGSGTNTREWKDYKAGFNLEREPWLNKDKTHLLTKSKEMTLRLDLEDF	300
Qy	301	NGLTLYALYDOFYVANEFLKYLRLHIGNTAGDALRESRHYNHDLRFTTTPDRDNDYRP	360
Db	301	NGLTLYALYDOFYVANEFLKYLRLHIGNTAGDALRESRHYNHDLRFTTTPDRDNDYRP	360
Qy	361	SGNGLYYSSGWDFDSCLSANLNGKYYHQYKGVYRNGIFWGTWPGINQAQPGYKSSFKQ	420
Db	361	SGNGLYYSSGWDFDSCLSANLNGKYYHQYKGVYRNGIFWGTWPGINQAQPGYKSSFKQ	420
Qy	421	AKMIRPKNEKP 432	

RESULT 6

RESULT 5

Biochemistry 33, 1988-1993, 1994

A>Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A;Pathway: blood coagulation
C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C;Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
F;341-355/Domain: calcium binding #status experimental
F;400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F;423-437/Region: platelet aggregation #status predicted
F;34/Dissulfide bonds: interchain (to gamma-35) #status experimental
F;35/Dissulfide bonds: interchain (to gamma-34) #status experimental
F;45/Dissulfide bonds: interchain (to beta-110) #status experimental
F;49/Dissulfide bonds: interchain (to alpha-64) #status experimental
F;78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;161/Dissulfide bonds: interchain (to beta-227) #status experimental
F;165/Dissulfide bonds: interchain (to alpha-180) #status experimental
F;179-208,352-365/Dissulfide bonds: #status experimental
F;424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status experimental
F;432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status experimental

Query Match 20.9%; Score 489.5; DB 1; Length 437;
Best Local Similarity 33.0%; Pred. No. 1.6e-27;
Matches 136; Conservative 53; Mismatches 25; Indels 69; Gaps 17;

QY 50 GSOCPPQL---TLPITLTIOPLROGLSMEEVKLEVRTLKEAVDSLKKSCDCKLQADDDR 105
||| ||| : : : : : | : : : : : | : : : : : | :
Db 42 GSYCTTCGTADFLSTYTQTVDKLQSLIEDILHOVENKTSEVKOLIKAIQ-LIYNPDSS 100
||| ||| : : : : : | : : : : : | : : : : : | :
QY 106 DPGNGGNGAGTAEDSRVQELESQVNKLSSELKNAKDQIQGLGRLETLHLVNNNTENY 165
||| ||| : : : : : | : : : : : | : : : : : | :
Db 101 KP-----NMIDAATLKSKMLE-EIMKYEASILTHDSIRYLQ-----EIYNSNN---- 144
||| ||| : : : : : | : : : : : | : : : : : | :
QY 166 VDNKANLVTVVNSLDGCKSCPKSQEHMQSOVVOHLYIKCSHDHYVLGRSSSGAYRVTPD 225
||| ||| : : : : : | : : : : : | : : : : : | :
Db 145 --QRIVNLKEKVAOLEAQCOB-PCKDTVFQ---IHDTGKDCQDIANKGAKOSGLYFIKPL 198
||| ||| : : : : : | : : : : : | : : : : : | :
QY 226 HRNSSFEVYCDMETMGGWTLQARLDGSTNFTREWVDYKAGFNLE----REPWLGNDK 281
||| ||| : : : : : | : : : : : | : : : : : | :
Db 199 KANQOFLVYCEIDSGNGWTFVQRDLGSDVDFKANNIYQREGFGHLSPTGTTEFWLGNEK 258
||| ||| : : : : : | : : : : : | : : : : : | :
QY 282 IHLTKSKEM--ILRIDLEDNFLTYALXDQFYVANEFLKRYLHIGNY-NGTAGDAL-- 336
||| ||| : : : : : | : : : : : | : : : : : | :
Db 259 IHLISTQSAIPYALRVELEDNWGRSTADYAMFKVGPEADKYRLTYAFAGGDAGDAFDG 318
||| ||| : : : : : | : : : : : | : : : : : | :
QY 337 -----RFSRIYHNIDLRFHTTPDRNDNRYPGNCGLYYSSGWDFDCLSANLNGKYY 387
||| ||| : : : : : | : : : : : | : : : : : | :
Db 319 FDFGDPSDKP--FTSHNGMFQFTWDNDNDKF-BGNCAEQDGSGWMNKCHAGLNGVYY 375
||| ||| : : : : : | : : : : : | : : : : : | :
QY 388 H-----QKYKGYRNIGFNGTWPIGNOAPGGYKS---SFKOAKMMIRPN 429
||| ||| : : : : : | : : : : : | : : : : : | :
Db 376 QGGTYKASTPNGYDNGLIINATW-----KTRWYSMKTKTTMIIFPN 416
||| ||| : : : : : | : : : : : | : : : : : | :

RESULT 7
FGRUGB
fibrinogen gamma-B chain precursor - human
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A>Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113,'I',115-453 <RIX>
A:Cross-references: GB:M1014; GB:J00134; GB:J00135; GB:X00086; NID:g182438; PIDN:AAB
R:Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A>Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near

A:Reference number: A92448; MUID:85030379
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Wolfenstein-Todel, C.; Mosesson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068993
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434, 'Y', 436-440, 'Z', 442, 'Z', 444, 'B', 446-447, 'R', 449, '2BB', 453 <WOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:88217900
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453 <FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tencchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334
A:Accession: I37390
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate splicing, which makes this chain different from the gamma-B chain at positions 434-437 and 438-440.
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plasma.
C:Genetics:
A:Gene: GDB:FGG
A:Cross-references: GDB:l19132; OMIM:134850
A:Map position: 4q28-q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGH) and two sets of beta chains. Two three-chain coiled coils emerge from this core and coiled into the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into fibrin.
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein; fibrin; fibrinogen; fibrinogen beta/gamma homology
F:1-26/Domain: signal sequence status predicted <SIG>
F:176-453/Product: fibrinogen beta-gamma chain #status experimental <MPT>
F:341-355/Domain: calcium binding #status predicted <FGB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of fibrinogen
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:49/Disulfide bonds: interchain (to alpha-64) #status predicted
F:78/Binding site: sulfate (Tyr) (covalent) #status experimental
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-160) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status predicted

Query Match 20.9%; Score 489.5; DB 1; Length 453;
Best Local Similarity 33.0%; Pred. No. 1.7e-27;
Matches 136; Conservative 53; Mismatches 154; Indels 69; Gaps 17;
QY 50 GSOCFFQL---TLPTLTQLPRLGSMEEVLKEVTLKEAVDSLAKSCQDCKLQADHR 105
DB 42 GSYCPTTCGIADFLSYQTKDKDQLQSLDELILHQVENKTSYKQLKATQ-LTYNPDSS 100
QY 106 DPGNGNGGAETAEDSRVCELESQVKNLSSELKNADQLOGRLETLHLVNMNIENY 165

Db 101 KP-----NMIDAATLKSRKMLE-EIMKYEASILTTHDSSIRYLQ-----EIYNSNN----- 144
QY 166 VDNKVALTVVNSLDGKSCPCPSOEHMQSQVQHLIYKDCSDHYVLGRSSGAVRTPD 225
Db 145 --QKIVNLKKEVALEAOQOE-PCADTVQ---IHDTGKDCQDIANKAKQSGLFYIPL 198
QY 226 HRNSFEYCYDMETMGCGVTLQARLDGSTNFTREWKDYKAGFGNLE-----REFWLGNDK 281
Db 199 KANQOFLVYCEIDGSGNGWTFVQKRLDGSVDKFNWIKYQKEGFGHLSPTGTTFFWLGNEK 258
QY 282 IHLTKSKEM-ILRIDLEDNGLTYLYDOFYVANFELKYRLHIGNY-NOTAGDAL-- 336
Db 259 IHLISTQSAIPALRVELEDWNGRTSTADYAMFKYGPADKYRLTYAYFAGGDAGDADG 318
QY 337 -----RFSRHYNHDLREFTTDRNDRYPCNGCLYYSSGWWFSCLSANLNGKY 387
Db 319 FDFGDDPSDKF--FTSHMGQFSTWDNDNDF-EGNCAEQDQSGWMNKNCHAGLNGVY 375
QY 388 H-----QYKYGVRNGIFWGTWPGINQAQPGYKS---SEKQAKWMIRPKN 429
Db 376 QGGTYSKASTPENGDIWATW-----KTRWYSMKTTMKIIPFN 416
RESULT 8
A25052
N:Contains: fibrinogen beta chain - sea lamprey (fragments)
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
R:Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BOH>
R:Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 428-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A:Reference number: A03120; MUID:77065679
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide bonds; blood coagulation; glycoprotein; sulfoxide
F:1-36/Product: fibrinopeptide B #status experimental <FPE>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:90-219/Domain: fibrinogen disulfide ring homology <FDR>
F:229-477/Domain: fibrinogen beta/gamma homology <FGB>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 20.1%; Score 470.5; DB 2; Length 479;
Best Local Similarity 30.5%; Pred. No. 4.1e-26;
Matches 133; Conservative 65; Mismatches 161; Indels 77; Gaps 14;
QY 39 PARLEGSGRCGSGCQPFQTLPTLTQLPRLGSMEEVLKEVTLKEAVDSLAKSCQDCK 98
Db 73 PQEAQKAIRDEGG-C--MLPESDLGVLCPTGTCLERELLKQRPVRYIKMLKQNLTYFI 129
QY 99 LQADDDHRDPGNGNGGAETAEDS-----RVCELESQVKNLSSELKNADQLOGRLE 153
Db 130 NSFD-----RMSDSNTLKNQVOTLRRRLNRSRSTHVNQKEI---ENRYKE 173
QY 154 LHLVNMNIENYVDNKVANLTVVVNSLDGKSCK-----CPSQEHMQSQ-----VOHLIY 203
Db 174 VKI-----RIESTVAGLSRSMKSVLEHLRAKMQRMEEATKTQELCSAPCTVNCRPVYSG 229

QY	204	KCSDHVLGRSSGAYRVT	PDHNRSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKD	263
Db	230	MHCEDIYRNGRRTSEAYIQ	PDLFSEPKVFCDMESHGGGWTVVQNRVDGSSNFARDWNT	289
QY	264	YKAGFG	-----NLREPMICNDKTHLLTKSKEMILRLTDLEDFNGLTLYALYDOF	312
Db	290	YKAEFGNIAFGNGKSCIN	IPGEYWLGTKVTHQLTKOHTQOVLFDMSDWGGSSVAYQYASF	349
QY	313	YVANEEFLKYRLHIGNTAG	DALRFSRHV-----NHDLRFETTPDRDNDRY----	359
Db	350	RPNEAOGYRLWEDYSGN	AGNALLEGATQLMGDNFTWTHNGMOFSTFDRDNDWNPCD	409
QY	360	PSGNCGLIYSSGWNFDS	CISANLNGKY-----HOKYKGVNRGIFWTGPGINOAPG	412
Db	410	PTKHCREDAGGWYNR	CHAANPNRGYIYWGVIYTKEQADYGTDDGVVWNNKVG-----S	463
QY	413	GYKSSPFQAKWMIRPK	428	
Db	464	WY--SMRQMAWKLRPK	477	
RESULT 9				
S05313				
fibrinogen gamma-B chain precursor - bovine				
C:Species: Bos primigenius taurus (cattle)				
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999				
C:Accession: S05313				
R:Brown, W.M.; Dziedzic, K.M.; Foreman, R.C.; Saunders, N.R.				
Nucleic Acids Res. 17, 6397, 1989				
A:title: Nucleotide and deduced amino acid sequence of a gamma subunit of b				
A:Reference number: S05313; MUID:89366676				
A:Accession: S05313				
A:Molecule type: mRNA				
A:Residues: 1-444 <BRO>				
A:Cross-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350				
A:Note: the authors translated the codon ACT for residue 105 as Ala and ATT				
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology				
F;1-24/Domain: signal sequence #status predicted <SIG>				
F;25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>				
F;174-414/Domain: fibrinogen beta/gamma homology <FBG>				
Query Match 19.9%; Score 466; DB 2; Length 444;				
Best Local Similarity 31.4%; Pred. No. 7.7e-26;				
Matches 138; Conservative 53; Mismatches 159; Indels 90; Gaps				
QY	36	AACPARGSGRC	-----EGSOCPQL-----TLPILTTLQPLQSGMDEVLEKVTTLKE	85
Db	20	SACLAYVATRDNCILDER	FGSYCPTTCGTADFLNNYQTSVKDLRTLEGILYQVENKTS	79
QY	86	AVDSLKSCODCKLQADHR	DPGGNGGAETASDRVOLESOVNKLSELKNKAKDQIQ	145
Db	80	EARELVKAIQ	-----ISYNPDQSPKNNISATYKNSKSMME	115
QY	146	GLQGRLEFTHLVNMMNT	-----ENYVDN-----KVALLTVVNSLDGCKSCKPSQEHMOSQPQV	199
Db	116	EIM-KYETLISTHETIR	FLEQYEVNSQKIVNLRDKVQVLEANCQF-PCQDTPVK-----IH	170
QY	200	HLIYKCDSDHYVLGRSS	GAYRVTDPHNRNSFEVYCDMETMGGGWTVLQARLDGSTNFTFR	259
Db	171	DVTGRDCQDVANKG	ESGLYFIRP-LKAKQFTLVYCEIDGSGNGWTVFQKRLDGSLDFKK	229
QY	260	EWKDYKAGFGNL	-----EREFWLGNDKIHLLTKSEM-----ILRLDLEDFNGLTLYALYDQ	311
Db	230	NWQYKEGFGHLSP	TGNTGNTFEWLNQEKIHLISTQSISPTVLRQLIEDWNGRSTADYAS	289
QY	312	FYVANEEFLKYRLHIGN	-NGTAGDAL-----RFSRHHNHLDRFTFTPDNRDNDRY	359
Db	290	FKVTGENDKYRLTVAY	FIGDAGDAPGDYDFGDDSDKFE--FTSHNGMQFSTWSDSDNKY	347
QY	360	PSGNCGLIYSSGWNFDS	CISANLNGKYH-----OKYKGVNRGIFWTGPGINOAPG	412

A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080
A:Contents: disulfide bonds
A:Accession: A94309
A:Molecule type: protein
A:Residues: 31-112, E', 114-137, 'QS', 140-144, 'QF', 147-148 <BLO>
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A:Reference number: A54223; MUID:94162201
A:Accession: G54223
A:Molecule type: protein
A:Residues: 164-174 <KUN>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370
A:Contents: annotation; review, disulfide bonds
R:Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A:Title: Primary structure of human fibrinogen. Characterization of disulfide-contains
A:Reference number: A91249; MUID:77245999
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA.
A:Reference number: A90038; MUID:83254384
A:Contents: annotation
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH
A:Reference number: A37117; MUID:90337977
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemateria ghilianii, the giant South American le
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FGB
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-4q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyrogutamic
F:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
F:31-49/Product: fibrinogen beta chain #status experimental <MAT>
F:31-44/Product: fibrinopeptide B #status experimental <APT>
F:45-49/Product: fibrin beta chain #status experimental <FGB>
F:45-47/Region: polymerization site
F:99-228/Domain: fibrinogen disulfide ring homology <FDR>
F:238-487/Domain: fibrinogen beta/gamma homology <FBG>
F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
F:95/Disulfide bonds: interchain (to alpha-55) #status experimental

F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:231-316,241-270,424-437/Disulfide bonds: #status experimental
F:394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.8%; Score 463; DB 1; Length 491;
Best Local Similarity 28.4%; Pred. NO. 1.4e-25;
Matches 131; Conservative 60; Mismatches 151; Indels 120; Gaps 13;

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RESULT 13
FGBOB
fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
C:Accession: A03122; B03117; B37507; A37513; S024#3
R:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.

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R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrino-
A;Reference number: A37513; MUID:81199473
A;Accession: A37513
A;Molecule type: mRNA
A;Residues: 44-468 <CHU>
R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads
A;Reference number: S02443; MUID:88211875
A;Accession: S02443
A;Molecule type: protein
A;Residues: 373-374 <MED>
C;Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopept
C;Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (C
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C;Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoxprotein
F;76-205/Domain: fibrinogen disulfide ring homology <FDR>
F;215-464/Domain: fibrinogen beta/gamma homology <FBG>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;371/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 19.6%; Score 458; DB 1; Length 468;
Best Local Similarity 28.5%; Pred. No. 3.1e-25;
Matches 123; Conservative 57; Mismatches 150; Indels 102; Gaps 11;

```

RESULT# 14
JH0675
restrictin precursor - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0675; PS0385; S23254
R:Noerenberg, U.; Wille, H.; Wolff, J.M.; Frank, R.; Rathjen, F.G.
Neuron 8, 849-863, 1992
A:Title: The chicken neural extracellular matrix molecule restrictin: similar

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A:Reference number: JH0675; MUID:92265298
A:Accession: JH0675
A:Molecule type: mRNA
A:Residues: 1-1353 <NOE>
A:Cross-references: GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
A:Experimental source: brain
A:Accession: PS0385
A:Molecule type: protein
A:Residues: 579-586;827-840 <NOE1>
A:Comment: This protein is a neural extracellular matrix protein implicated in neural cell adhesion.
A:Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibrinectin type I
C:Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprotein
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-1353/Product: restrictin #status predicted <MAT>
F:234-229/Domain: EGF homology <EG1>
F:234-260/Domain: EGF homology <EG2>
F:265-291/Domain: EGF homology <EG3>
F:296-322/Domain: EGF homology <EG4>
F:324-405/Domain: fibrinectin type III repeat homology <FN1>
F:413-494/Domain: fibrinectin type III repeat homology <FN2>
F:502-584/Domain: fibrinectin type III repeat homology <FN3>
F:592-676/Domain: fibrinectin type III repeat homology <FN4>
F:684-764/Domain: fibrinectin type III repeat homology <FN5>
F:772-853/Domain: fibrinectin type III repeat homology <FN6>
F:861-941/Domain: fibrinectin type III repeat homology <FN7>
F:949-1027/Domain: fibrinectin type III repeat homology <FN8>
F:1035-1115/Domain: fibrinectin type III repeat homology <FN9>
F:1130-1338/Domain: fibrinogen beta/gamma homology <FBG>
F:1272-1286/Region: calcium binding #status predicted
F:53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn)

Query Match 19.4%; Score 454.5; DB 1; Length 1353;
Best Local Similarity 41.0%; Pred. No. 2.1e-24;
Matches 94; Conservative 33; Mismatches 83; Indels 19; Gaps 6;

QY 204 KDCSDHYLVGRSSGAYRTPD--HRNSSFFVYCDMETMGGGWTVLQRLDGTFTREWK 262
DB 1131 QDCAQHLMGNDTLGVTYISINGDLSQVQVFCDMSTDGGWIVFORRQGLTDFRQWA 1190
QY 263 DYKAGGNLERERWLGNDKHLTKSKEMILRDLDFNLGLTYALYDQFVANEFLKYR 322
DB 1191 DYRVGFGNLEDFWGLDNLHKITSQRYELRDMRD--GQEAAYAYYDKFSGDSRSLYK 1249
QY 323 LHGTNYNGTAGDALRSRHHYHDLRFTTPDRNDRYPSGNCGLYSSGWWFDSCLSANL 382
DB 1250 LRIGDTNGTSGDSLTY-----HGRPFSTKDRND--VAVTNCAMSYKGAWYKNCHEHTNL 1303
QY 383 NGKYHOKYKGVNRNGIFWGTWPGINOAQPGYKSSFKQAKMIRPNKFK 431
DB 1304 NGKYGESRHS--QGYNWYHWK-----GHEFSIPFVEMKRPYNYHR 1341

RESULT 15
D44234
fibrinogen alpha chain precursor, extended splice form - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide A
C:Species: Homo sapiens (man)
C>Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
C:Accession: D44234; B44234
R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redman
Biochemistry 31, 11968-11972, 1992
A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A:Reference number: D44234; MUID:93090725
A:Accession: D44234
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA; DNA
A:Residues: 1-866 <FU1>
A:Cross-references: GB:M58569; NID:g182406; PID:g182407
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
A:Accession: B44234
A:Molecule type: mRNA; DNA

A:Residues: 605-866 <FU2>
A:Note: sequence extracted from NCBI backbone (NCBIP:119917)
C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: See PIR:FGHUA for the major splice form. It is not known whether this form
C:Genetics:
A:Gene: GDB:FGA
A:Cross-references: GDB:119129; OMIM:134820
A:Map position: 4q28-4q28
A:Introns: 18/3; 60/3; 122/1; 171/2
A:Note: the list of introns is incomplete
C:Complex: The fibrinogen molecule is a hexamer containing two sets of three nonident
ntained in the core. Two three-chain coiled coils emerge from this core and connect i
distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C:Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F:36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F:57-185/Domain: fibrinogen disulfide ring homology <FDR>
F:591-593/Region: cell attachment (R-G-D) motif
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
F:55/Disulfide bonds: interchain (to beta-95) #status experimental
F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
F:68/Disulfide bonds: interchain (to beta-106) #status experimental
F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
F:184/Disulfide bonds: interchain (to beta-223) #status experimental
F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F:322/Cross-link: isopeptide (Lys) (interchain to alpha-2-plasmin inhibitor 41-Gln) #
F:347,385/Cross-link: isopeptide (Gln) (interchain to alpha) #status experimental
F:461-491/Disulfide bonds: #status experimental
F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to alpha) #status pred
F:686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 454; DB 2; Length 866;

Best Local Similarity 39.4%; Pred. No. 1.3e-24;

Matches 102; Conservative 41; Mismatches 74; Indels 42; Gaps 11;

QY 192 HMQSOPVOHLIYKDCSDHYVL----GRSSGAYRTPDHRNSSFFVYCDMETMGGGWTVL 247

DB 623 HAKSRPV-----RDCDD--VLQTHPSGTQSGIFNKLPGSSKIFSVYCDQETSLGGLLI 675

QY 248 QARLDGSTNFTREWKYKAGFNL----ERFPLGNDKHLTKSKEMILRDLDFENGL 303

DB 676 QQRMDGSLNFNTWQDYKRGFGLNDEGEFNLGHLTLQ--RGSVLRVLEEDWAGN 734

QY 304 TLYALDYFVANEFLKYRLHIGNYNGTAGDAL-----RFSRHHYHDLRFTTPDRND 357

DB 735 EYAEY-HFRVSEAEAGALQVSSYEGTAGDALIEGSEVEGAEYTSNNMQSTEDRAD 793

QY 358 RYPSGNCGLYSSGWWFDSCLSANLNGY-----HOKYKGVNRNGIFWGTWPGINQ 408

DB 794 QWEE-NCAEYVGGWYNNCAAANLNGIYYPGGSYDPRNNSPYE-IENGVVWVSFRGADY 851

QY 409 AQPGGYKSSFKQAKMIRP 427

DB 852 -----SLRAVRMKIRP 862

Search completed: February 27, 2001, 12:50:13

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:38 ; Search time 30.15 Seconds
(without alignments)
489.941 Million cell updates/sec

Title: US-09-442-143-4

Perfect score: 2340

Sequence: 1 MRLPGWLSSAVLAACRAV.....GYKSFQKQMMIRKPKFKP 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq/AA1985.DAT:*
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8: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT:*
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16: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2340	100.0	432	W88236	Mouse prothrombina
2	1853.5	79.2	439	W88235	Human prothrombina
3	537.5	23.0	499	W47529	Amino acid sequenc
4	533.5	22.8	314	R65759	Rat hepatic parench
5	533.5	22.8	496	W01411	Human TIE-2 ligand
6	533.5	22.8	496	W47529	Human TIE-2 ligand
7	533.5	22.8	496	W47532	Human TIE-2 ligand
8	533.5	22.8	496	W47532	Human angiotensin
9	533.5	22.8	496	W47528	Human angiotensin
10	528	22.6	498	W47528	Amino acid sequenc
11	524	22.4	312	W47528	Hepatocyte prolif
12	522	22.3	312	W47528	Hepatocyte prolif

13	521	22.3	312	15	R65760	Human hepatic pare
14	507	21.7	346	20	Y23736	Human AR-1 protein
15	507	21.7	346	20	Y05399	Human TIE ligand N
16	494.5	21.1	461	21	Y66727	Membrane-bound pro
17	494.5	21.1	496	19	W47527	Amino acid sequenc
18	493	21.1	495	21	W78904	Angiotensin fusio
19	493	21.1	495	21	W78907	Angiotensin fusio
20	490	20.9	494	19	W47526	Amino acid sequenc
21	489.5	20.9	497	17	W01410	Human TIE-2 ligand
22	489.5	20.9	497	17	R94604	Human TIE-2 ligand
23	489.5	20.9	497	19	W47531	Amino acid sequenc
24	489	20.9	498	17	W01409	Human TIE-2 ligand
25	489	20.9	498	17	R94603	Human TIE-2 ligand
26	489	20.9	498	19	W47530	Amino acid sequenc
27	489	20.9	498	21	W78902	Human angiotensin
28	489	20.9	498	21	W78905	Human angiotensin
29	488.5	20.9	453	16	R82245	Human fibrinogen g
30	488.5	20.9	453	16	R82246	Human fibrinogen g
31	488	20.9	491	20	Y26196	Human zapo3 protei
32	488	20.9	491	20	Y05397	Human TIE ligand N
33	488	20.9	491	21	Y69483	Amino acid sequenc
34	488	20.9	491	21	Y68761	An angiotensin-re
35	483.5	20.7	493	20	Y05396	Human TIE ligand N
36	483.5	20.7	493	21	Y70745	PSEQ-3 protein enc
37	483.5	20.7	493	21	Y54999	Human scarface 1 p
38	483	20.6	491	21	Y44841	Human secreted pro
39	480.5	20.5	411	16	R84650	Fibrinogen gamma c
40	476.5	20.4	509	19	W47533	Amino acid sequenc
41	474.5	20.3	509	19	W26792	Mouse TIE-2 recept
42	470	20.1	503	19	W47534	Amino acid sequenc
43	470	20.1	503	19	W26791	Human TIE-2 recept
44	470	20.1	503	20	Y23735	TIE ligand-4 (TL4)
45	465.5	19.9	454	16	R84551	Partial human fibr

ALIGNMENTS

RESULT 1

W88236
ID W88236 standard; Protein; 432 AA.

XX W88236;

XX AC
XX DT 15-MAR-1999 (first entry)

XX Mouse prothrombinase Fgl2 protein.

XX Prothrombinase; Fgl2; mouse; immune coagulation; antibody;
XX inhibitor; infection; graft rejection; glomerulonephritis; cancer;
XX gastrointestinal disease; foetal loss; therapy; vaccine.

XX Mus sp.

XX Key Location/Qualifiers
XX Modified-site 172..174

FT Modified-site /label= Asn is N-glycosylated
FT Modified-site 228..231
FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 256..259
FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 323..325
FT Modified-site /note= "Asn is N-glycosylated"

FT Domain
FT Domain /note= "fibrinogen related domain"

W09851335-A1.

19-NOV-1998.

15-MAY-1998; 98WO-CA00475.

10-OCT-1997; 97US-0061684.

applicant

PR	15-MAY-1997;	97US-0046537.	
XX	(LEVY/) LEVY G.		
XX	Levy G;		
XX	WPI; 1999-059687/05.		
DR	N-PSDB; V84140.		
XX	Modulating immune coagulation - by using Fgl2 antibodies and		
PT	compounds, used to treat conditions including graft rejection and		
PT	foetal loss		
XX	Claim 8; Page 70-71; 105pp; English.		
XX	This is the amino acid sequence of mouse prothrombinase Fgl2, as		
CC	predicted from fgl2 DNA (see V84140). Fgl2 is a 70 kDa		
CC	transmembrane serine protease that has immune procoagulant activity.		
CC	The human Fgl2 amino acid sequence is given in W88236. The		
CC	invention provides a method for inhibiting immune coagulation by		
CC	inhibiting the activity or expression of Fgl2. The method can be		
CC	used in vivo to treat a condition which requires a reduction in		
CC	immune coagulation such as bacterial and viral infections, cancer,		
CC	glomerulonephritis, a number of gastrointestinal diseases,		
CC	allograft and xenograft rejection and foetal loss. An Fgl2-specific		
CC	antibody, an Fgl2 antisense oligonucleotide, or a substance that		
CC	affects prothrombinase activity of a Fgl2 protein may be used to		
CC	treat a condition requiring a reduction in procoagulant activity.		
CC	A vaccine containing an Fgl2 protein or peptide is used for		
CC	prevention of graft rejection or foetal loss (claimed).		
XX			
XX	Sequence 432 AA;		
QY	Query Match 100.0%; Score 2340; DB 20; Length 432;		
	Best Local Similarity 100.0%; Pred. No. 2.2e-199;		
	Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps		
QY	1 MRLPGWLWSAVLAACRAVEEHNLTGEGLEDSAAQAACPARLEGSGRCGSGCPQLTLP 60		
DB	1 mrlpgwlwssavlaacraveehnltegieledsaqaacparlegsgrcsgcpqfqltlp 60		
QY	61 TLATQLPRLGSMEEVLKEVRTLKEAVDSLKKSCDCKLQADHRDPGNGNGAETAED 120		
DB	61 tltqiqlrgsmeevlkevertlkeavdslkkscdqcklqadhrdpngngngaetaed 120		
QY	121 SRVOELESQVKNLSSELKNAKDOIQLGRLETLHLVNMNNIENYVDNKVANLTVVVNSL 180		
DB	121 srvgelsgvknlsiselknakddiqglqgrletlhlvnmnnienyvdnkvantlvvvnsl 180		
QY	181 DGKCKCPSOEHMQSOPVQHLIYKDCSDHVYLGRRSSGAYRVTPDHRNSSFEVYCDMETM 240		
DB	181 dgkckscpsgehmqspvqhlllykdcsdhyvlgrrssgayrvcpdhrnssfevycdmetm 240		
QY	241 GGGWTVTLQARLDGSTNFTREWKDYKAGFGNLEREFVLGNDKIHLLTKSEMILRIDLEDF 300		
DB	241 gggwvtvlqarldgstnftrewkdykagfgnlerefvlgndkihilcksemilridledf 300		
QY	301 NGLTLYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHYNHDILRFPTTPDRDNDRYP 360		
DB	301 ngltlyalydqfyvaneflkyrlhignyngtagdalrfsrhyndhrlrfttppdrndndryp 360		
QY	361 SGNGCLYSSGWWFSDCLSANLKGYYHQYKGVNRGIFWGTWPGINQAQPGGYKSSFFKQ 420		
DB	361 sgncglyssgwwfdscslsanlkgyyhkykgyngifwgtwpginqapggysfsfkq 420		
QY	421 AKMIRPKNFKP 432		
DB	421 akmairpknfkp 432		

RESUIT, T
W88235
2

```

Query Match          79.2%; Score 1853.5; DB 20; Length 439;
Best Local Similarity 77.7%; Pred. No. 3.2e-156;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;
QY 1 MRLPGWLWSSAVLAACR-AVEEHNLTGLEDASAQAACPARLEGSGRC-BGSOCPPFLT 58

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```

Db 1 mklanywysavlatyglvanneteekderakadvprlesrdkceagcpqvs 60
QY 59 LPTLTQLPRLQSGMEVLEKVRTLKAVDSLAKKSCODCKLQADHRDPGNG---GNG 114
Db 61 lplltlqlpkqfsrievefkeqnlkeivnsllkscqcklqaddngdpgrngllpstdg 120
QY 115 AE-TAEDSRVQLESOVNKLSSSLKNAKQIOGLOGRLETLHLVNMNNIENYDNKYANL 173
Db 121 apgevgnrvrelesevnklsselknaakeeinvlgrleklnlvnmnnienyvdskvanl 180
QY 174 TVVNSLDGCKSCPKSQEHMQSOPVQHLYKDCSDHYVLGRRSGAVRTPDRHNSFEV 233
Db 181 tfvnsldgckscpsqeqqlsqrpvghlykdcsvyagkrsetyrvtpdpknssfev 240
QY 234 YCDMETMGSGWTVLQARLDGSTNFTREWKDYKAGFGLNERFEWLGNDKIHLLTKSEKIL 293
Db 241 ycdmetcmgggwtvlgarlsgstnfttwgdykagfgnlrrefwlgndkhlitkskemil 300
QY 294 RIDLEDFNLGLTYALYDOFYVANEFLKYLRIHIGNYTAGDALRFSRHYNHLRFFTTTPD 353
Db 301 ridledfngvlyalydyfyvaneefkylrhvgnngtagdalrnfkhnhdklffttpd 360
QY 354 RNDRYPSGNGLYSSGWNFDSCLSANLNGKYYHOKYKGVNRNGIFWGTWPGINQAOPGG 413
Db 361 knddrypsngcglyssgwwfdacslsanlngkyyhkyrgvrgngifwgtwpgvseahpgg 420
QY 414 YKSSFKQAKMMIRPKNFKP 432
Db 421 ykssfkakmmirpkhfkp 439

```

RESULT 3

W47529
ID W47529 standard; Protein; 499 AA.

XX AC W47529;

XX DT 09-SEP-1998 (first entry)

XX DE Amino acid sequence of chimeric TIE ligand IN2C2F (chimera 3).
XX KW Chimeric TIE ligand IN2C2F; TIE-2 ligand; neovascularisation;
XX KW tumour; human.

XX OS Homo sapiens.

XX PN WO9805779-A1.

XX PD 12-FEB-1998.

XX PF 01-AUG-1997; 97WO-US13557.

XX PR 25-OCT-1996; 96US-0740223.

XX PR 02-AUG-1996; 96US-0022999.

XX PA (REG-) REGENERON PHARM INC.

XX PI Davis S, Yancopoulos GD;

XX DR WPI; 1998-145615/13.

XX DR N-PSDB; V18616.

XX PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
XX PT healing

XX PS Claim 20; Fig 26; 202pp; English.

XX CC This is the amino acid sequence of the chimeric TIE ligand IN2C2F,
XX CC used in the method of the invention, involving the production
XX CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
XX CC and host cells used in the method of the invention are useful for
XX CC the recombinant production of the ligands. The ligands, etc. are

CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.

XX SQ Sequence 499 AA;

Query Match 23.0%; Score 537.5; DB 19; Length 499;
Best Local Similarity 28.4%; Pred. No. 2.2e-39;
Matches 149; Conservative 83; Mismatches 165; Indels 127; Gaps 19;

```

QY 7 LWLSSAVLAACRAVBEHNLTEGLEDAQAACPARLEGSG---RCEGSCQPFQLTLP-- 60
Db 3 vflsfafiala-----lth--igcsnqrsp---ensgrrynriqhgqccaytilpeh 50
QY 61 -----TUTIQLPRLQSGMEVLEKVRTLKEAV-----DSLKK 92
Db 51 dgncresttdgynntalqrdaphvdpdsvqlrvlenimennntqwmklennyiqdnmkk 110
QY 93 SCQCKLQADHR-----DPGGNGNGAETAEDSR-VQELSEQV----- 130
Db 111 emveiqgnavnqntavmieigtlnln--qtaeqtrkltdveaqvlnqtrrlqllehs 168
QY 131 --NKLSSSELKNAKQIOGLOGR-----LETLHLVNMNNIENYVDN--KVANLTV 175
Db 169 sthkleqildqtseinklqdknsflekvvlamedkhlilqisikeekdqlqvlvskqns 228
QY 176 VVNSLDGKC-----SKPCSQEHMQSOPVQHLL-----YKDCS 207
Db 229 lileekkivtatvnnsvlqkqhdmetvnnlmtmstnsakdptvakeeqisfrdca 288
QY 208 DHYVLGRRSSGAYRTPDRHNSFEVCDMETMGSGWTVLQARLDGSTNFTREWKDYKAG 267
Db 289 evfksghhtnglyltlfpnsteeikaycdmeagggwtliqrredgsvdqfqtwekykv 348
QY 268 FGNLEREFMLGNDKIHLTKSEKILRIDLEDFNLGLTYALYDOFYVANEFLKYLRIHGN 327
Db 349 fgnpsgeyglnefvsqitngqvivkhlkdwegneayslyehfysseelnyrihkg 408
QY 328 YNGTAGDALRFSRHYNHLRFFTTDRDNDRYPSGNGCGLYSSGWNFDSCLSANLNGKYY 387
Db 409 ltgtagkissisqpgnd----fstkdgndkci-cksqmltggwvfwfdaacpsnngmy 463
QY 388 HOKYKGVNR-NGIFWGTWPGINQAOPGGYKSSFKQAKMMIRPKNF 430
Db 464 pqrqntnkfngikwywkg-----sgy--slkattmmirpadf 499

```

RESULT 4

R65759
ID R65759 standard; protein; 314 AA.

XX AC R65759;

XX DT 17-MAY-1995 (first entry)

XX DE Rat hepatic parenchymal cell growth factor.

XX KW Hepatic parenchymal cell growth factor; HPGF; liver diseases;
XX KW liver cancer; cirrhosis.

XX OS Rattus rattus.

XX FH Key Location/Qualifiers

XX FT Peptide 1..24

XX FT /label= sig_peptide

XX PN WO9421678-A.

XX PD 29-SEP-1994.


```

AC R94605;
XX
DT 28-OCT-1996 (first entry)
XX
DE Human TIE-2 ligand 2 derived from pBluescript KS clone.
XX
KW Angiogenesis; neovascularisation; tumour development; wound healing;
KW TIE; tyrosine kinase with Ig and EGF homology domains; vector;
KW recombinant; clone; diagnosis; ischaemia; thromboembolytic disease;
KW atherosclerosis; inflammation; diabetes; ligand bodies; delivery;
KW targeting.
XX
OS Homo sapiens.
XX
PN WO9611269-A2.
XX
PD 18-APR-1996.
XX
PF 06-OCT-1995; 95WO-US12935.
XX
PR 06-APR-1995; 95US-0418595.
PR 07-OCT-1994; 94US-0319932.
PR 27-OCT-1994; 94US-0330261.
PR 02-DEC-1994; 94US-0348492.
PR 09-DEC-1994; 94US-0353503.
PR 17-JAN-1995; 95US-0373579.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Aldrich TH, Bruno J, Davis S, Goldfarb M, Jones PF;
PI Maisonnier PC, Radziejewski C, Yancopoulos GD;
XX
DR WPI; 1996-209850/21.
DR N-PSDB; T14650.
XX
PT Nucleic acid encoding TIE-2 ligand and related vectors - useful in
PT diagnosis and treatment of neovascularisation, tumours, etc., or to
PT promote wound healing, etc.
XX
PS Claim 2; Fig 6; 84pp; English.
XX
CC R94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript
CC KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions
CC of the native ligand coding sequences and may be used to produce the
CC ligands at a high yield. Antibodies and receptor bodies that bind to
CC TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation
CC (e.g. associated with tumour development) and the TIE-2 ligands
CC themselves are useful to promote neovascularisation and wound healing
CC e.g. for treatment of ischaemia. TIE-2 ligands are also useful to
CC treat thromboembolytic disease, atherosclerosis, inflammation and
CC diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for
CC the delivery and targeting of growth factors, toxins etc. to sites
CC where their presence is advantageous.
XX
SQ Sequence 496 AA;

Query Match 22.8%; Score 533.5; DB 17; Length 496;
Best Local Similarity 29.4%; Pred. No. 4.9e-39;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CSGSQCPF-----QLTLPITLTLPLQLGSMEEVLKE----VPTLKEAV-DSLKKSCQDC 97
Db 53 crssspysvnavqadpleyddsqrqlvlenimntqwmklnyiqdnmkkenvel 112
QY 98 KIQADDHR-----DPGGNGNGAETAEDESR-VOELESQV-----NKL 133
Db 113 qnavqngqtavmiegtlhn--qtaeqtrkitdveaqlnqttrlelqllehslnk 170
QY 134 SSELKNAKDQIQLOGR-----LETLHLVNNNIENYVDN---KYANLTVVVVNSL 180
Db 171 ekqildqtseinkldqnsflekvvamedkhhiiqlsqikeekdqqlvlskqnsiieel 230

QY 181 DGKC-----SKCPSQEHMQSQPVQOHLI-----YKCDSDHYVL 212
Db 231 ekkiatvtnnsvlqkqghdmetvnnlltmnstsnsakdptvakeeqisfrdcaevfks 290
QY 213 GRRSSGAYRVPDHRNSSFEVYCDMETGGGTVVLOARLDGSTNFTREWKDYKAGFGNLE 272
Db 291 ghtnnglytlftpnsteeikaycdmeaggwvliqrredgsdvtqrwkeykvdfgnps 350
QY 273 REFVLGNDKIHLLTKSKEMILRIDLEDFENGLTLYALYDOFYVANEFKLYRLHIGNYNGTA 332
Db 351 geywlgnefvsltnqqrqvikihihkwegneayseyehfyisseelnyrihiklgtgta 410
QY 333 GDALFRSRHYNHDLRFFTPDRDNDRYPGNGCLYSSGWNFDSCLSANLNGKYHQRYK 392
Db 411 gkissisqpgnd----fstkdgndkcic-kcsqmltgwwfdacgpnslngmyypqrqn 465
QY 393 GVR-NGIFWGTWPGINQAQPGGYKSSFKQAKMMIRPKNF 430
Db 466 tnknfngikwywvkg-----sgy---slkattmmirpadf 496

RESULT 7
W47532
ID W47532 standard; Protein; 496 AA.
XX
AC W47532;
XX
DT 09-SEP-1998 (first entry)
XX
DE Human TIE-2 ligand 2 from clone pBluescript KS.
XX
KW Chimeric TIE ligand 2NIC1F; TIE-2 ligand; neovascularisation;
KW tumour; human.
XX
OS Homo sapiens.
XX
PN WO9805779-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13557.
XX
PR 25-OCT-1996; 96US-0740223.
XX
PR 02-AUG-1996; 96US-0022999.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
DR WPI; 1998-145615/13.
XX
DR N-PSDB; V18619.
XX
PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing
XX
PS Example 8; Fig 6; 202pp; English.
XX
CC This is the amino acid sequence of the human TIE-2 ligand 2,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
SQ Sequence 496 AA;

Query Match 22.8%; Score 533.5; DB 19; Length 496;
Best Local Similarity 29.4%; Pred. No. 4.9e-39;

```


PN WO200002584-A2.
XX 20-JAN-2000.
XX 12-JUL-1999; 99WO-US15600.
XX 13-JUL-1998; 98US-0094672.
PR 02-DEC-1998; 98US-0110608.
XX (TEXA) UNIV TEXAS SYSTEM.
XX PA
XX PI Thorpe PE, Ran S;
XX WPI; 2000-182175/16.
DR N-PSDB; 292215.
XX New composition for killing tumour vascular endothelial cells for
PT treating solid tumours, comprises unconjugated anti-aminophospholipid
PT antibody -
XX
PS Disclosure; Page 223-224; 226pp; English.
XX
CC This sequence represents the human angiotensin-2 (Ang-2) amino acid
CC sequence. Ang-2 is a naturally occurring angiogenesis antagonist when
CC vascular endothelial growth factor (VEGF) levels are low, and generally
CC counteracts the blood vessel maturation and stability mediated by Ang-1.
CC Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation
CC or stabilisation factor, converting immature vessels to mature vessels.
CC Both Ang-1 and Ang-2 are useful in a therapeutic approach to the
CC treatment of vascularised tumours. The invention relates to a composition
CC comprising an anti-aminophospholipid antibody, or its antigen binding
CC region. The composition is used to kill tumour vasculature endothelial
CC cells. Aminophospholipids are stable and specific markers accessible on
CC the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used
CC in the composition of the invention. The composition is used to treat
CC malignant or benign vascularised tumours in animals, especially large
CC tumours.
XX
SQ Sequence 496 AA;

Query Match 22.8%; Score 533.5; DB 21; Length 496;
Best Local Similarity 29.4%; Pred. No. 4.9e-39;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;
QY 48 CCGSQCP-----QLTLPITLTLQPLQSGMEVLKE-----VRTLKEAV-DSUKKSCQDC 97
Db 53 crssspyyvsnvqrdapleyddsvqrlqvlvlenimennntqwmklnyiqdnmkemvel 112
QY 98 KIQADDDR-----DPGGNGGNGAETAEADSR-VOELESQV-----NKL 133
Db 113 qgnvqngtavnleigtlnlln--qtaeqtrklcdvqvlngttrlelqllehlstnkl 170
QY 134 SSELKNAKDQIQGLQGR-----LETLHLVNNNIENYVDN---KVALTVVNVNSL 180
Db 171 ekqildqtseinkldqksnflekvlamedkhiqisikeekdqqlvlskqnsiieel 230
QY 181 DKGC-----SKCPSEQHEMQSQPVQVHLL-----YKDCSDHYVL 212
Db 231 ekkvitvatvnnsvlqkqhdmetvnnlmtmstnsakdptvakeeqisfrdcaevfks 290
QY 213 GRSSGAYVTPDHRNSSEVYCDMETMGGVTVLQARLDGNTFNFRWKDYKAGTGNLE 272
Db 291 ghtntgiyltfnsteeikaycdmeagggwtiqrredgsvdfgrtwkeykvfgnps 350
QY 273 REFWLGNDRKIHLLTKSKEMILRIDLFNGLTLYALYDQFYVANEFLLKYLRLHIGNYNGTA 332
Db 351 geywlgnervsqitnqrvyrlkhlkdwegneayslyehfyfssseelnryrlhkgitgta 410
QY 333 GDALFRSRYHNDLRFPTPPDRNDRPSGNGGLYSSGSGWFDSCLSANLNGKYYHQYK 392
Db 411 gkissisqpgnd----fstkdgdndkic-kesqmltgwfwfdacpsnlngmypyqrqn 465

QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKOAKMMIRPKNF 430
Db 466 tnknfngikwywkg-----sgy--slkattmmirpadf 496
RESULT 10
W47528
ID W47528 standard; Protein; 498 AA.
XX AC W47528;
XX 09-SEP-1998 (first entry)
XX Amino acid sequence of chimeric TIE ligand 1NIC2F (chimera 1).
DE Chimeric TIE ligand 1NIC2F; TIE-2 ligand; neovascularisation;
KW tumour; human.
XX Homo sapiens.
OS WO9805779-A1.
PN 12-FEB-1998.
PD 01-AUG-1997; 97WO-US13557.
XX 25-OCT-1996; 96US-0740223.
PR 02-AUG-1996; 96US-0022999.
XX (REGE-) REGENERON PHARM INC.
XX Davis S, Yancopoulos GD;
PI WPI; 1998-145615/13.
DR N-PSDB; V18615.
XX Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing
PT Claim 20; Fig 24; 202pp; English.
XX This is the amino acid sequence of the chimeric TIE ligand 1NIC2F,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
SQ Sequence 498 AA;
Query Match 22.6%; Score 528; DB 19; Length 498;
Best Local Similarity 31.8%; Pred. No. 1.5e-38;
Matches 140; Conservative 70; Mismatches 142; Indels 88; Gaps 17;
QY 19 AVEEHNL-----TEGLEDSASAQAACPARLBSGRCESQCPFOLTTLTTL-TIOLPRO-L 70
Db 119 avqhtatmleigtclslsqtaeqtrkltdvetqvlngtsrlelqllehlstykql 178
QY 71 GSMEVLK--EVRTL-----KEAVDSLKKSCQDCQLQADDDHDPGGNGGNGAE 116
Db 179 qgtneilkheksnllekhkilemegkheelditkeeknlq-----glv 223
QY 117 TAEDSRVOELESQVKNLSSELKNAKDQIQGLRLETLH-LVNNMNIENYVDNKNVATV 175
Db 224 trqyilqelekqinratt--nnsvlqkqgle-lmdtvhnlvnl----- 264
QY 176 VVNSLDKCKSK----CPSQEHMQSQPVQVHLLYKDCSDHYVLGRSSGAYRVTPDHRNSSF 231

SQ	Sequence	312 AA;
Query Match	22.4%;	Score 524; DB 17; Length 312;
Best local Similarity	37.8%;	Pred. No. 1.7e-38;
Matches 126;	Conservative 41;	Mismatches 114; Indels 52; Gaps
QY	112	NGAETAEDSRVQE--LESOVNKLSELKNAKDQIQGLQGRLFTLHLVNNNNIENYVDNK 169
DB	17	greisaledcaeqmrlraqvrlletrvk-----qqqvikqlqenevq-fldkg 56
QY	170	VANLTVVVNSLDCKSCPCSQEHMQSOPVOHLLIYKDCSDHYVLGRSSGAYRVTPDHRNS 229
DB	67	dentvvdlgs-----krq-----yadceifndgyklsghykikplqspa 106
QY	230	SFEVYCDEMTWGGGWTVLARLDGSTNFTREWDYKAGFNLER---EFWLGNDKIHLLT 286
DB	107	efsvycdmsd-gggwtviqrsgdsenfnrgwkdyengfngvqkhgeylgknlnhflit 165
QY	287	KSEMIILRIDLEFNGLTLVALYDOFYVANEFLKYRLHIGNYNGTAGDALRFSRH---- 341
DB	166	tqedytlikidafeknsryaqkfnkvdekbnfyelnigeysgtagdsagnfhpevw 225
QY	342	-YNHDLRFPTPDNDRYPSGNCGLYSYGSGWFDSCLSANLGKYIYHOKYKG-VRNGIF 399
DB	226	washqrmkfstwrdrdhny-egnceaedqsgwwfnrchsanlmgvyysgpytaktngiv 284
QY	400	WGTPWPGINQAOPGGYKSSFQAKMMIRPKNFKP 432
DB	285	wytw-----hgwwyslksvmkirpndfip 309
RESULT	12	
ID	R94316	standard; Protein; 312 AA.
XX	AC	R94316;
XX	AC	
DT	05-NOV-1996	(first entry)
XX	Hepatocyte proliferation substance HP-041.	
DE	Human hepatocyte proliferation substance; rat; probe; SR-alpha promot	
KW	chinese hamster ovary cell; CHO; hepatitis.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	Peptide	1..22
FT	/note= "signal peptide"	
FT	Protein	23..312
FT	/note= "mature protein"	
XX	WO9609383-A1.	
PN		
XX	28-MAR-1996.	
PD		
XX	21-SEP-1995;	95WO-JP01904.
PF		
XX	22-SEP-1994;	94JP-0228234.
PR		
XX	(TAIS) TAISHO PHARM CO LTD.	
PA		
XX	Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;	
PI		
XX	WPI; 1996-188445/19.	
DR	N-PSDB; T13396.	
DR		
XX	Vector for expression of hepatocyte proliferation substance - in	
PT	eukaryotic cells, used as diagnostic reagent for hepatitis and for	
PT	basic research on in vitro liver cell cultures	
PS	Claim 2: Page 23-24: 44pp: Japanese	

XX This is the amino acid sequence of a human hepatocyte proliferation
 CC substance (HPS). The gene encoding the HPS was isolated from a
 CC lambda-gt10 human cDNA library using a fragment of the corresp. rat gene
 CC as a probe (sequence not given in the specification). The human gene was
 CC cloned in plasmid pSCL to produce plasmid pSVLH which was subsequently
 CC recombined to produce plasmid pcDNA-dhfr in which the HPS gene is under
 CC control of the SR-alpha promoter. This plasmid is transformed into CHO
 CC cells to express the HPS protein. The HPS protein can be used to diagnose
 CC hepatitis.
 XX Sequence 312 AA;

Query Match 22.3%; Score 522; DB 17; Length 312;
 Best Local Similarity 37.5%; Pred. No. 2.5e-38;
 Matches 125; Conservative 42; Mismatches 114; Indels 52; Gaps 11;

QY 112 GNGAETAEADSRVQE--LESQVNLKSLKNAKDQIQGLGRLETLHLVNMNNIENYVDNK 169
 DB 17 greisaledcaeqmrlraqvrlletrvk-----qqgvkikqlqenevq-fldkg 66
 QY 170 VANLTVVNSLDGCKSCPSQEHMQSQPVQHLIYKDCSDHYVLGRSSGAYRVTPDHRNS 229
 DB 67 dentvidlgs-----krq-----yadceifndgkylsgfykikpqlqla 106
 QY 230 SFEVYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLT 286
 DB 107 efsyvcmdsd-99gwtvlgrrsdgsenfngwkdyengfngvqkhgelygnknlhfl 165
 QY 287 KSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYLRLHIGNYNGTAGDALRFSRH----- 341
 DB 166 tqedytlkidladfeknsryaqyknfkvgdekfnfynlgeysgtagslagnfhpevqw 225
 QY 342 -YNHDLRFTTTPDRNDRIYSGWFGWFDSCLSANLNGKYHYQYKYG-VRNGIF 399
 DB 226 washqrmkfstwdrdhny-egnceaedqsgwwfnrchsanlngvyygpytaktmgiv 284
 QY 400 WGTWPGINAOQPGYKSSFKQAKMMIRPKNFKP 432
 DB 285 wytw-----hgwwyslksvmmkirpndfip 309

RESULT 13
 R65760
 ID R65760 standard; protein; 312 AA.

XX R65760;
 XX
 XX
 XX 17-MAY-1995 (first entry)
 DE Human hepatic parenchymal cell growth factor.
 XX Hepatic parenchymal cell growth factor; HPGF; liver diseases;
 KW liver cancer; cirrhosis.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= sig_peptide

XX WO9421678-A.
 XX
 XX 29-SEP-1994.
 XX
 XX 22-MAR-1994; 94WO-JP00455.
 XX
 XX 23-MAR-1993; 93JP-0063905.
 XX
 XX (TAIS) TAISHO PHARM CO LTD.
 XX
 XX Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;

XX
 DR WPI; 1994-316940/39.
 DR N-PSDB; Q77819.
 XX
 PT Hepatic parenchymal cell growth promoter peptide - is isolated
 PT from human or animal liver cell or produced by recombinant
 PT techniques and used for therapy of liver diseases
 XX
 PS Claim 2; Page 34; 47pp; Japanese.
 XX
 CC Q77819 encodes R65760 rat hepatic parenchymal cell growth factor (HPGF).
 CC The protein or the N-terminal peptide (R65757) may be used in the
 CC diagnosis and treatment of liver diseases, such as liver cancer and
 CC cirrhosis.
 XX
 SQ Sequence 312 AA;

Query Match 22.3%; Score 521; DB 15; Length 312;
 Best Local Similarity 37.5%; Pred. No. 3.1e-38;
 Matches 125; Conservative 43; Mismatches 113; Indels 52; Gaps 11;

QY 112 GNGAETAEADSRVQE--LESQVNLKSLKNAKDQIQGLGRLETLHLVNMNNIENYVDNK 169
 DB 17 greisaledcaeqmrlraqvrlletrvk-----qqgvkikqlqenevq-fldkg 66
 QY 170 VANLTVVNSLDGCKSCPSQEHMQSQPVQHLIYKDCSDHYVLGRSSGAYRVTPDHRNS 229
 DB 67 dentvidlgs-----krq-----yadceifndgkylsgfykikpqlqla 106
 QY 230 SFEVYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLT 286
 DB 107 efsyvcmdsd-99gwtvlgrrsdgsenfngwkdyengfngvqkhgelygnknlhfl 165
 QY 287 KSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYLRLHIGNYNGTAGDALRFSRH----- 341
 DB 166 tqedytlkidladfeknsryaqyknfkvgdekfnfynlgeysgtagslagnfhpevqw 225
 QY 342 -YNHDLRFTTTPDRNDRIYSGWFGWFDSCLSANLNGKYHYQYKYGVRN-GIF 399
 DB 226 washqrmkfstwdrdhny-egnceaedqsgwwfnrchsanlngvyygpytaktmgiv 284
 QY 400 WGTWPGINAOQPGYKSSFKQAKMMIRPKNFKP 432
 DB 285 wytw-----hgwwyslksvmmkirpndfip 309

RESULT 14
 Y23736
 ID Y23736 standard; Protein; 346 AA.

XX Y23736;
 XX
 XX 08-SEP-1999 (first entry)
 XX Human AR-1 protein sequence.

XX Receptor tyrosine kinase; AR-1; angiogenesis regulator;
 KW neoplastic disease; tumour angiogenesis; wound healing;
 KW thromboembolic disease; atherosclerosis; inflammatory disease;
 KW AR-1 receptor.

XX Homo sapiens.
 XX
 XX WO9932639-A1.
 XX
 XX 01-JUL-1999.
 XX
 XX 17-DEC-1998; 98WO-US26800.
 XX
 XX 19-DEC-1997; 97US-0994309.
 XX
 XX (REGE-) REGENERON PHARM INC.

XX PI Valenzuela DM;
XX XX
XX WPI; 1999-418933/35.
DR N-PSDB; X85783.
XX
XX Receptor tyrosine kinase, AR-1 and related nucleic acid molecules
XX
XX Example 4; Fig 4A-B; 50pp; English.
XX
XX The present sequence represents a receptor tyrosine kinase, designated
XX AR-1, which is related to TIE ligands. AR-1 is believed to be a
XX regulator of angiogenesis and thus the factor, as well as nucleic acids
XX encoding it, are useful in the diagnosis and treatment of certain
XX diseases such as neoplastic diseases involving tumour angiogenesis,
XX wound healing, thromboembolic diseases, atherosclerosis and inflammatory
XX diseases. AR-1 can also be used to support the survival and/or growth
XX and/or migration and/or differentiation of human AR-1 receptor expressing
XX cells. AR-1 can be used to identify the AR-1 receptor. AR-1-cytotoxic
XX conjugates can be used to target tumours expressing AR-1 or its receptor.
XX Antagonists of AR-1, e.g. antibodies are useful to prevent or attenuate
XX its biological activity.
XX
XX Sequence 346 AA;

Query Match 21.7%; Score 507; DB 20; Length 346;
Best Local Similarity 35.5%; Pred. No. 6.4e-37;
Matches 123; Conservative 54; Mismatches 121; Indels 48; Gaps 14;
QY 104 HRDPGGNGGNGAETADSRVQELSQVNLKSELK--NAKDOIQGLQGRLETLHL-VNMN 160
Db 32 hktpaqqlkaanccee--vkelkaqvanlssllselakkqrdwsvvmqvmlesnksk 89
QY 161 NIENYVDNKVANLTVVVNSLDGKCKSPQEHMQSOPVQHL-----IYKDCSDHYVLG 213
Db 90 rmesrltadaeskysemnngid-----lmqlaaqtvtqttsadaily-dcsslyqkn 138
QY 214 RRSSGAYRVTPDH--RNSSEFYVCDMETMGGGWTVLOARLDGSTNFTREWKDYKAGFGNL 271
Db 139 yrisgvyklppddflgspelvfdcmetsgggwtliqrksglvsvfydwkqykgfgsi 198
QY 272 EREFWLGNDKTHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYNGT 331
Db 199 rgdfwlgnehlrlsrqptr-lrvemedwegnlryaeshfvlglnelsyrlflgnytn 257
QY 332 AG-DALFRSRHYNHDLRFFTPDRDNDRYPSGNCGLYSSGWWFSDCLSANLNGKYY--- 387
Db 258 vngdaly-----hntatstkdndnc-lkcaqlrkgygwyncctdsnlngvyrylg 311
QY 388 -HOKYKGVNRNGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNFKP 432
Db 312 ehkh---ldgitwygwhgsty-----slkrvmekirpedfip 346

RESULT 15

ID Y05399 standard; Protein; 346 AA.
XX
AC Y05399;
XX
XX 01-JUL-1999 (first entry)
XX Human TIE ligand NL4 protein sequence.
XX
KW Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis;
KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KW early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KW endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KW vasculogenesis; detection; diagnosis; therapy.
XX
OS Homo sapiens.
XX

PN W09915653-A2.
XX
XX PD 01-APR-1999.
XX
XX PF 14-SEP-1998; 98WO-US19093.
XX
XX PR 29-OCT-1997; 97US-0960507.
XX PR 19-SEP-1997; 97US-0933821.
XX
XX PA (GETH) GENENTECH INC.
XX
XX PI Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;
XX PI Hillan K, Roy M, Schwall R, Tumas D;
XX
XX DR WPI; 1999-263480/22.
XX DR N-PSDB; X36344.
XX
XX PT New isolated TIE ligand homologs for, e.g. developing products for
XX PT treatment of tumors
XX
XX PS Claim 8; Fig 14; 132pp; English.
XX
XX CC This sequence is the human tyrosine kinase containing Ig and EGF
XX CC homology domains (TIE) ligand of the invention, designated NL4.
XX CC The TIE receptors are receptor tyrosine kinases which are expressed in
XX CC vascular endothelial cells and early haemopoietic cells. The TIE
XX CC receptors are believed to be actively involved in angiogenesis, and may
XX CC play a role in haemopoiesis as well. The TIE ligand homologs can promote
XX CC the survival and/or growth and/or differentiation of TIE receptor
XX CC expressing cells. They can be used for promoting neovascularisation in
XX CC wound healing and for promoting angiogenic processes, such as for
XX CC inducing collateral vascularisation in an ischaemic heart or limb, or for
XX CC promoting bone development and/or maturation of growth in a patient
XX CC or muscle growth and development. The TIE ligand homologs and antibodies
XX CC can inhibit the growth of endothelial cells and induce apoptosis of
XX CC cells, particularly tumour cells. They can inhibit vasculogenesis,
XX CC particularly the vascularisation of tumour cells. The antibodies can also
XX CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,
XX CC NL8 or NL4 polypeptide is amplified. The products can also be used for
XX CC detection, diagnosis, drug screening and production of transgenic
XX CC animals.
XX
XX SQ Sequence 346 AA;

Query Match 21.7%; Score 507; DB 20; Length 346;
Best Local Similarity 35.5%; Pred. No. 6.4e-37;
Matches 123; Conservative 54; Mismatches 121; Indels 48; Gaps 14;
QY 104 HRDPGGNGGNGAETADSRVQELSQVNLKSELK--NAKDOIQGLQGRLETLHL-VNMN 160
Db 32 hktpaqqlkaanccee--vkelkaqvanlssllselakkqrdwsvvmqvmlesnksk 89
QY 161 NIENYVDNKVANLTVVVNSLDGKCKSPQEHMQSOPVQHL-----IYKDCSDHYVLG 213
Db 90 rmesrltadaeskysemnngid-----lmqlaaqtvtqttsadaily-dcsslyqkn 138
QY 214 RRSSGAYRVTPDH--RNSSEFYVCDMETMGGGWTVLOARLDGSTNFTREWKDYKAGFGNL 271
Db 139 yrisgvyklppddflgspelvfdcmetsgggwtliqrksglvsvfydwkqykgfgsi 198
QY 272 EREFWLGNDKTHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYNGT 331
Db 199 rgdfwlgnehlrlsrqptr-lrvemedwegnlryaeshfvlglnelsyrlflgnytn 257
QY 332 AG-DALFRSRHYNHDLRFFTPDRDNDRYPSGNCGLYSSGWWFSDCLSANLNGKYY--- 387
Db 258 vngdaly-----hntatstkdndnc-lkcaqlrkgygwyncctdsnlngvyrylg 311
QY 388 -HOKYKGVNRNGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNFKP 432
Db 312 ehkh---ldgitwygwhgsty-----slkrvmekirpedfip 346

Search completed: February 27, 2001, 12:48:40
Job time: 65 sec

SPTREMBL 15: *

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1853.5	79.2	439	4	Q14314	Q14314	homo sapien
2	630.5	26.9	652	5	Q9NDQ1	Q9NDQ1	ciona intes
3	541.5	23.1	375	6	Q77802	Q77802	bos taurus
4	534	22.8	495	4	Q9P2Y7	Q9P2Y7	homo sapien
5	533.5	22.8	496	4	Q15123	Q15123	homo sapien
6	532	22.7	407	13	Q9PU54	Q9PU54	gallus gal
7	524.5	22.4	444	4	Q9NRR7	Q9NRR7	homo sapien
8	519.5	22.2	312	4	Q08830	Q08830	homo sapien
9	513.5	21.9	292	5	Q9U8W8	Q9U8W8	tachypneus
10	507	21.7	346	4	Q43827	Q43827	homo sapien
11	506	21.6	496	11	Q35608	Q35608	mus musculus
12	489.5	20.9	435	13	Q93568	Q93568	gallus gal
13	489	20.9	498	4	Q15389	Q15389	homo sapien
14	488	20.9	491	4	Q95841	Q95841	homo sapien
15	483.5	20.7	493	4	Q9UKU9	Q9UKU9	homo sapien
16	482	20.6	308	5	Q908W6	Q908W6	tachypneus
17	480.5	20.5	498	11	Q08538	Q08538	mus musculus
18	480	20.5	493	11	Q9R045	Q9R045	mus musculus
19	479	20.5	316	5	Q9U8W7	Q9U8W7	tachypneus

1 MRLPGWLWSSAVLAACR-AVEEHNLTGLEDASQAACPARLEGSQY

1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDASQAACPARLEGSGRC-EGSQCPFQLT 58

Query Match	23.1%	Score 541.5	DB 6	Length 375
Best Local Similarity	33.7%	Pred. No. 1.2e-32		
Matches	128	Conservative 53	Mismatches 116	Indels 83
Gaps				
QY 116	ETAEDSR-VQLESQV-----	-----NKLSSSELKNAKQIQGLQGR-----	150	
	: : : : :	: : : : :		
Db 14	QTAEQTRKLTDEAQLVNOTTRLELQQLLEHSLSTNKLKQILDQTSISKLDQKNSFLEK 173			
QY 151	----LETLHLVNNNNNIENYVD-----	-----NKVAN-----LTVVNSLDGCKSKCPSQE 191		
	: : : : :	: : : : :		
Db 74	KVLDMEDKHIVQLRSIKEEKDQLQVLVSKONSIEELEKQLVTFVNN-----SVLQKQQ 128			
QY 192	HMSQPYOHL-----	-----IYKDCSDHYVLGRSSSGAYRVTPDHRNSSF 231		
	: : : : :	: : : : :		
Db 129	HDLMETVNNLLTLMSTSNPSYLLAKNDEQIIFRDCGEAFKSGLTTSVVTLTFPNSTEEI 188			
QY 232	EVYCDMETMGGWTVLQARLDGSTNFTREWQYKAGFNLEREFWLGNDKIHLLTTSKEM 291			
	: : : : :	: : : : :		
Db 189	KAYCDMETGGGWTVIQRRDEGSDVFQRTWKKEYKVGFGNPSGEHVLGNEFVSQVTGQKRY 248			
QY 292	ILRLDLEDEGLTLYALYDOQFYVANELKYLRHLHGNYNTAGDALRFSRHYNHDLRFFTT 351			
	: : : : :	: : : : :		
Db 249	VLKIHLDKWDGNGENRAYSUFDYLSNEELNRIHLGLGTAGKISSISQPGND-----FST 304			
QY 352	PDQNDRYPGNGCLGYSSGWFSDCLSANLNGKYYHQYKGYR-NGIFWGTPWPGINQAO 410			
	: : : : :	: : : : :		
Db 305	KDADNDKIC-KCSQMLTGWFEDACGPNLNGMYYPQONTNKFNGIKWYWKG----- 358			
QY 411	PGYKSSFKQAKMWRPKNF 430			
	: : : : :	: : : : :		
Db 359	-SGY--SLKATTMMIRPADF 375			
RESULT 4				
Q9P2Y7	PRELIMINARY;	PRT; 495 AA.		
ID AC	Q9P2Y7			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)			
DE	ANGIOPOIETIN-2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RA	Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,			
RA	Wands J.R.;			
RT	"Biologic significance of angiotensin-2 expression in human			
RT	hepatocellular carcinoma."			
RL	J. Clin. Invest. 103:341-345(1999).			
DR	EMBL; AB009865; BAA95590.1.			
SQ	SEQUENCE 495 AA; 56848 MW; EBFAC35ABFI08F6 CRC64;			

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Query Match      22.8%; Score 534; DB 4; Length 495;
Best Local Similarity 29.5%; pred. No. 6.3e-32;
Matches 135; Conservative 80; Mismatches 153; Indels 90; Gaps 16;

QY 48 CEGSQCPF-----QUTLPTLTQLPRQLSGMEELVKE-----VRTLKEAV-DSLAKKSCOD 97
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 CRSSSPFVSNVAVORDAPLEYDDSVQRLQVLNEMNTQWLKLENYIQDNMKKEMVEI 112
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 98 KLAQDDR-----DPGGNGGNGAETADSR-VOELESQV-----NKL 133
      : | :: | | | | | | | | | | | | | | | | | | | | |
Db 113 QQNAVQNOTAVMIEIGYNLLN--QTAETRKLTDVEAQVLNQTRLEQLLEHSLSTNKL 170
      : | :: | | | | | | | | | | | | | | | | | | | | |
QY 134 SSELKNAKDQIOGLQGR-----LETLHLYNMNINIYVDN---KYANLTVVYNSL 180
      : | :: | | | | | | | | | | | | | | | | | | | | |
Db 171 EKQILQDTSETNKLDKRNNSFLKKVLAEMDKHIITQLOSIKEERQDQVLVYSKQNSIIEEL 230
      : | :: | | | | | | | | | | | | | | | | | | | | |

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Qy	191	DGKC-----SKCPSEHQMSQVQHLLI-----YKDCSDHYVLG 210 : :
Dq	231	EKKVTATVNNSLQKHLDLMETVNNLLTMMSTSNKSDFVAKEEQISFRDCAEYFKSG 1 : :
Qy	214	RSSGAYRVTPDHRSNSSFVCMDMETGGGTWVQLARLDGSTFTREWDKYRAGFONLER 273 : :
Dq	291	HTTGNGITLTLPNSTEIRKAYCDMEAGGGMTIIORREDGSVDFFRTWKYEYKVGFNPGS 350 : :
Qy	274	EFWLGNDKIHLLTKSEMILRIDLEENGLTYALYDOFYVVANEEFLRYHLHIGNYNGTAG 333 : :
Dq	351	EYWLGNFEVSOLTNQORYVLKIHLKDWEANEASLYEHFYLSEEELNYRIHLKGLTGTAG 410 : :
Qy	334	DALRFSRHHNHDLRFPTTDNDNDRYPSGNCGLYYISGWWFDSCLSANLNKYYYHQYKYG 393 : :
Dq	411	KISSISPQGD----FSTKDGDNCKIC-KCSQMLTGGWWFDACGPSNLNGMYYPQRONT 465 : :
Qy	394	VR-NGIPWGCTPGINOAQPGRGYKSSPFQAOKWMIRPNKF 430 : :
Dq	466	NKFNIGIKRWYKVG-----SGY--SLKATTMMIRPADF 495 : :
RESULT	5	
O15123		PRELIMINARY; PRT; 496 AA.
ID	O15123	
AD	O15123;	
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DE	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	ANGIOPOLETIN-2.	
GN	ANGPT2.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OC	NCBTaxId=9606;	
RN	[]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LUNG;	
RX	MEDLINE=97349327; PubMed=9204896;	
RA	Maisonnier Pierre C.; Suri C.; Jones P.F., Bartunkova S., Wiegand S.J.,	
RA	Radziejewski C., Compton D., McClain J., Aldrich T.H.,	
RA	Papadopoulos N., Daly T.J., Davis S., Salo T.N., Yancopoulos G.D.;	
RT	"Angiopietin-2, a natural antagonist for Tie2 that disrupts in vivo	
RT	angiogenesis.";	
RL	Science 277:55-60(1997).	
CC	-1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL	
CC	MATURATION/STABILITY MEDIATED BY ANGIOPOLETIN-1 (ANG-1). ITS	
CC	FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC	
CC	INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX	
CC	CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT	
CC	VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE	
CC	ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A	
CC	PERMISSIVE ANGIOGENIC SIGNAL.	
CC	-1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF	
CC	THE BETA AND GAMMA CHAINS OF FIBRINOGEN.	
DR	EMBL; AF004327; AAC63190.1; .	
DR	HSPSP; P02671; 1FZD.	
DR	MIM; 601922; .	
DR	INTERPRO; IPR002181; .	
DR	PFAM; PF00147; fibrinogen_c_1.	
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.	
KW	Coiled coil.	
FT	DOMAIN 55 58 POLY-SER.	
FT	DOMAIN 130 256 COILED COIL (POTENTIAL).	
FT	DOMAIN 282 496 FIBRINOGEN BETA/GAMMA.	
FT	DOMAIN 318 321 POLY-GLY.	
SQ	SEQUENCE 496 AA; 56919 MW; 5642A58847A7385C CRC64;	
Query Match	22.8%; Score 533.5; DB 4; Length 496;	
Best Local Similarity	29.4%; Pred.No. 6.9e-32;	
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps		
Qy	48	CBSQCPCF-----OLTUPLTIQLPRLGSMEEVLKE---VRTLKAEV-DLSLKSCODC 97

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Db 53 CRSSSPVSVNAVQDAFLDYDDSVQRLOVLENNENFTQWLKLENYLODNKKKEWVEI 112
QY 98 KQADDIR-----DPGGNGNGAETAEDSR-VOELESQV-----NKL 133
Db 113 QONAVONQTAVMIEGTGTLN--QTAEQTKLTDVEAQVLAQTTRLEQLLHLSLSTNKL 170
QY 134 SSELKNKADQIOGQGR-----LETLLHVNMIENIYVDN---KVALTVVVSLSL 180
Db 171 EKQILDQSETINKLODRNFKLEKKVLAEMDKHIIQLOSIKEKDQQLVLSKONSIIIEEL 230
QY 181 DGKC-----SKCPSQBHMOSQPVQHLI-----YKDCSDHYVL 212
Db 231 EKKIVTATVNSVLQKQOQDLMETVNNLLTMWSTNSAKDPTVAKEEQISFRDCAEVFS 290
QY 213 GRRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFNLE 272
Db 291 GHTTNGIYTLTFPNSSTEEIKAYCDMEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPS 350
QY 273 REFVLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYTA 332
Db 351 GEYWLGNFEVSQLTNQQRVVLKHLKDWEGNEAYSLEYEHFVLSSEELNYRIHLKGLTGA 410
QY 333 GDALRFSHYNDLRFPTTDRNDYRPSGNCGLYSSGWFFDSCLSANLNGKYYHOKYK 392
Db 411 GKISSIQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYTPQRON 465
QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 466 TNKFNKGIKYYWKG-----SGY--SLKATMMIRPADF 496

RESULT 6
Q9PU54 PRELIMINARY; PRT; 407 AA.
ID AC Q9PU54
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-OCT-2000 (TREMREL. 15, Last annotation update)
DE ANGIOPOIETIN-2 (ANG-2B).
GN ANGIOPOIETIN-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HUBBARD WHITE MOUNTAIN;
RA Mezquita J., Mezquita B., Pau M., Mezquita C.;
RT "Characterization of a novel form of angiotensin-2 (Ang-2B) and
RT expression of vEGF and angiotensin-2 during chicken testicular
RT development and regression."
RL Biochem. Biophys. Res. Commun. 260:492-498(1999).
DR EMBL; AJ31923; CAB59200.1; -.
DR HSSP; P02671; IFLD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen_C.1.
DR PROSITE; PS00514; FIBRINAG_C_DOMAIN.1.
SQ SEQUENCE 407 AA; 46647 MW; E10C03D07E410013 CRC64;

Query Match 22.7%; Score 532; DB 13; Length 407;
Best Local Similarity 33.8%; Pred. No. 6,9e-32;
Matches 136; Conservative 62; Mismatches 130; Indels 74; Gaps 14;

QY 63 TIQPLRQIGSME-EVLKEVRLTKEAVDSLKSCQDCKLQADPHRDPGGNGNGAETAEDS 121
Db 46 TAEQTKLTDVEAQVLAQVLTTRLE--LQLEHLSLSTNKLQK-----ISVQTNIT 93
QY 122 RVQE-----LESQVNLSE-----LKNKADQIOGQGRLETLHLVNNMIENYVDNKV 170
Db 94 KQEKNSFLKRVLEMDKHTLQLKSINDEKQDLQVLAR-----QNSIIELEKQL 145
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QY 171 ANLTVVNSLDGKCKCPCSQEHMQSQPVQHLI-----YKDCSDH 209
Db 146 --VTATVNN-----SVLQKQOQDLMETVNNLLTMISTPNSAKNFIAKEQISFKDCAEA 198
QY 210 YVLRGSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFG 269
Db 199 FRSGLTTSYTYLTFPNSAQEKKAYCDMESNGGWTVLRREGGSDVDFHRTWEYKIGFG 258
QY 270 NLREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYN 329
Db 259 DPAGEWLGNFEVSQLTNQQRVVLKHLKDWEGNEAYTLYDQFYLANEEOKYRIHLKGLT 318
QY 330 GTAGDALRFSHYNDLRFPTTDRNDYRPSGNCGLYSSGWFFDSCLSANLNGKYYHQ 389
Db 319 GTAGKISSIQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYPL 373
QY 390 KYGVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 374 QNNKFNKGIKYYWKG-----SGY--SLKATMMIRPADF 407

RESULT 7
Q9NR7 PRELIMINARY; PRT; 444 AA.
ID AC Q9NR7
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMREL. 15, Last annotation update)
DE ANGIOPOIETIN-2 ISOFORM-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiotensin-2."
RL J. Biol. Chem. 275:18550-18556(2000).
DR EMBL; AF187858; AAF76526.1; -.
SQ SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;

Query Match 22.4%; Score 524.5; DB 4; Length 444;
Best Local Similarity 34.6%; Pred. No. 2.8e-31;
Matches 118; Conservative 57; Mismatches 119; Indels 47; Gaps 9;

QY 116 ETAEDSRVOELESQVKN--LSSE-----LKNKADQIOGQGRLETLHLVNNMIEN 164
Db 125 QTSEINKLQDKNSFLEKKVLAEMDKHIIQLOSIKEEKDQQLVLSK-----QNSIIE 176
QY 165 YVDNKVANLTV-----VVNSLDGKCKCPCSQEHMQSQPVQHLIYKDCSDHY 210
Db 177 ELEKKIVTATVNSVLQKQOQDLMETVNNLLTMWSTNSAKDPTVAKEEQISFRDCAEVF 236
QY 211 VLGRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFGN 270
Db 237 KSHHTNGIYTLTFPNSSTEEIKAYCDMEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGN 296
QY 271 LEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYN 330
Db 297 PSGEYWLGNFEVSQLTNQQRVVLKHLKDWEGNEAYSLEYEHFVLSSEELNYRIHLKGLTG 356
QY 331 TAGDALRFSHYNDLRFPTTDRNDYRPSGNCGLYSSGWFFDSCLSANLNGKYYHQ 390
Db 357 TAGKISSIQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYTPQ 411
QY 391 KYGVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 412 QNTNKNFNGIKYYWKG-----SGY--SLKATMMIRPADF 444
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RESULT 8
Q08830 PRELIMINARY; PRT; 312 AA.
AC Q08830;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR.
GN HFREP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=HEPATOMA;
RX MEDLINE=93290661; PubMed=8390249;
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
RT related gene, HFREP-1."
RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
CC - SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
CC - TISSUE SPECIFICITY: OVEREXPRESSED IN HEPATOCELLULAR CARCINOMAS.
CC - SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL; D14446; BAA03336.1;
DR HSSP; P02671; 1F2D.
DR INTERPRO; IPR002181;
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Plasma; Blood coagulation; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 312 FIBRINOGEN-LIKE PROTEIN 1.
FT SIMILAR 70 296 BETA/GAMMA CHAINS OF FIBRINOGEN.
FT DISULFID 83 112 BY SIMILARITY.
FT DISULFID 248 261 BY SIMILARITY.
FT SEQUENCE 312 AA; 36378 MW; 2330F3D60CD0B8A CRC64;
SQ
Query Match 22.2%; Score 519.5; DB 4; Length 312;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 131; Conservative 47; Mismatches 117; Indels 93; Gaps 11;
QY 55 FOLTPLTLTQLPRLGSMEEVLKEVTLKAEVDSLAKSCQDCKLQADDDHDPGNGNG 114
DB 5 FSPILVTALINGREISALEDCAOEQMLRAQVRL----- 40
QY 115 AETAEDSRVOELESQVKNLSSELKNNAKDOIQLOGRETLHLVNMNNTENYVDNKVANLT 174
DB 41 -----ETRYKQOQVKIKQLQE-----NEVQFL-----DKGDEDT 70
QY 175 VVYNSLDGKCKPCSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVY 234
DB 71 VW--DLGSRQ-----YADCEIFNDGYKLSGYFKIKPLQSPAESFSVY 111
QY 235 CDNETGGGTVQLARLDGSTNTREWKQYKAGFNLER---EFWLNKDIHLITKSKEM 291
DB 112 CDMSD--GGGTWTVIQRSDSGENFRGKKDYENGFGNFGVQKHGFWLGNKLNHLFTTQEDY 170
QY 292 ILRIDLEDFNGLTYALYDQFYVANEFLKYLHIGNYGTAGDALRFSRH-----YNHD 345
DB 171 TLKIDLADEFKNRYAQYKFKVDEKNFYELNIGESYGTAGDSLGNFHPVOMWASHQ 230
QY 346 LRFPTTPDRNDNRYPSGNCGLIYSSGWFDFSCLSANLNGKYKHQYKYG--VRNGIFWGTWP 404
DB 231 RMKFSTWDRDHDNY--EGNCAEEDQSGWFRNCHSANLNGVYISGPYTAKTGNGIWTW-- 288
QY 405 GINQAPGGYKSKFQAKMMIRPKNFKP 432
DB 289 -----HGWSYLSKSVVMKIRPNDFIP 309
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RESULT 9
Q090W8 PRELIMINARY; PRT; 292 AA.
AC Q090W8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TECHLECTIN-5A.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
RA Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
RT immunity are structurally related to fibrinogen."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL; AB024737; BAA84188.1;
DR HSSP; P02671; 1F2D.
DR INTERPRO; IPR002181;
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;
SQ
Query Match 21.9%; Score 513.5; DB 5; Length 292;
Best Local Similarity 42.7%; Pred. No. 1.1e-30;
Matches 103; Conservative 38; Mismatches 81; Indels 19; Gaps 6;
QY 195 SQPVQHLIYKDCSDHYVLGRRSSGAYRVTPDH--RNSSEVYCDMETGGGWTVLQAR-- 250
DB 61 AQPIYSPDPTCADILLNGYRSGGYRIWPKSWMTVGLNVCYCDMETDGGGWTVIORRG 120
QY 251 -LDGSTNFTREWKQYKAGFNLEREFWLNKDIHLITKSKEMILRIDLEDFNGLTYALY 309
DB 121 YGNPSDIYFKPKNYKLGEGNIEKDFWLNGRIFALTNRQNYMIRFDLKDENDTRYAIY 180
QY 310 DQFYVANEFLKYLHIGNYGTAGDALRFSRHYNHDLRFTTPDRNDNRYPSGNCGLIYYS 369
DB 181 QDFWIENEDYLYCLHIGNYSGDAGNS--FGRHNGH--FSTIDKDHDTHT--HCAQTYK 234
QY 370 SCWWFDSCLSNLNGKYKHQYKGYRNGIFWGTWPCINQAOQPGYKSKFQAKMMIRPKN 429
DB 235 GGMWYDRCHESNLNGLYNGEHSYADGIEWRAWK-----GYHSLPQVEMKIRPVE 286
QY 430 F 430
DB 287 F 287
RESULT 10
Q43827 PRELIMINARY; PRT; 346 AA.
AC Q43827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CDT6.
GN DJ647M16.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CORNEA;
RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
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Query Match 20.9%; Score 489.5; DB 13; Length 435;
Best Local Similarity 31.8%; Pred. No. 1.4e-28;
Matches 136; Conservative 51; Mismatches 140; Indels 101; Gaps 17;

QY 50 GSQCP-----FQLA-----LPTLTQLPQLGSMEEVLKEVRLTKEAVDSLK 91
DB 42 GSYCPTTCGTADFNKYLRTTDEGLLELLQQAQWSTSGSIEYLQHIKTI----- 93
QY 92 KSCQDCKLQADHRDPGGNGGGAETAEDSRVQLESQVNLKSLSEKNAKDQIQLOGLR 151
DB 94 -----YPSKQTLPOSIEQLTQSKKILIEII-----RY 122
QY 152 ETUHLVNMNINIYVD-----NKVANLTVVNSLDGKSKCPQSEHQSPVQVHLKYD 205
DB 123 ENTILAHENTIOQLTDMHIMNSNKKITQKQIAQLESCHQEB-PCKD--TAEIQETGRD 178
QY 206 CSDHYVLGRSSGAYRVTDPHRNSSFEVYCDMETMGGWTVLQARLDGSGTNFTREWKDY 265
DB 179 CQDIANKGARKSGLYFIKQAKQSFVLYCEIDTYGNGWTVLQRLDGSDFRNWVQYK 238
QY 266 AGFNGLE---REFWLGNDKIHLLTSKEM--ILRIDLEFNGLTLYALYDQFYVANEFL 319
DB 239 EGFHGLSPDDTTEFWLGNEXIHLITQSTLPYALRIELEDWSGKKGTADYAVFKVGTED 298
QY 320 KYRL-----HIGNYNGTAGDALRF-----SRHYNHDLRFTTTPDRNDRYPSGNCGLY 368
DB 299 KYRLTYAYFTIGGERGDAFCDFNFGDDPSDKSYTHVNGMR-FSTPDNDNF-EGNCAEQD 356
QY 369 SSGWFDSCLSANLNGYY----HOKYGYR---NGIFWGTWPGINAOAGGYKSSPKQA 421
DB 357 GSGWMNRCCHAGLNGPYIIGGYVSRDTGNTSDNGIITATW-----RDRWY--SMKKT 408
QY 422 KMIIRPKN 429
DB 409 TKMLIIFN 416

RESULT 13
Q15389 PRELIMINARY; PRT; 498 AA.
AC Q15389;
DC Q15389;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-1 (ANG-1).
GN ANGPT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FETAL LUNG;
RX MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonpierre P.C.,
RA Vancopoulos G.D.;
RA "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning.";
RL Cell 87:1161-1169(1996).
RN [2]
RP SEQUENCE OF 307-498 FROM N.A.
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RA "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RL DNA Res. 1:27-35(1994).
RN [3]
RP SEQUENCE OF 307-498 FROM N.A.
RX MEDLINE=96051389; PubMed=7584028;
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RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1 (supplement).";
RL DNA Res. 1:47-56(1994).
CC -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -!- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC ISCHEMIC HEART.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
CC -!- PTM: GLYCOSYLATED.
CC EMBL: U83508; AAB50557.1; -
CC EMBL: D13628; BAA02793.1; -
CC HSP; P02671; IEPD.
CC MIN; 601667; -
CC INTERPRO; IPR002181; -
CC PFAM; PF00147; fibrinogen.C.1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil.
FT DOMAIN 81 119 COILED COIL (POTENTIAL).
FT DOMAIN 153 261 COILED COIL (POTENTIAL).
FT DOMAIN 284 498 FIBRINOGEN BETA/GAMMA.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match 20.9%; Score 489; DB 4; Length 498;
Best Local Similarity 31.1%; Pred. No. 1.4e-28;
Matches 137; Conservative 70; Mismatches 145; Indels 88; Gaps 17;

QY 19 AVEEHNL-----TEGLEDAQAACAPARLEGSGCEGSCQCFOLTPLTL-TIQLPRO-L 70
DB 119 AVQNHTATMLEIGTSLLSQTABQTRKLTDTVETQVNLTSRLIEIQLLENSLSYKLEKQL 178
QY 71 GSMEVLK--EVRTL-----KEAVDSLKKSCQDCKLQADHRDPGGNGGAE 116
DB 179 QOTNEILKIHENKSLLEHKELEMECKHKEELDTLKEENLQ-----GLV 223
QY 117 TAEDSRVQELSESQVNLKSLSEKNAKDQIQLOGLRLETLH-LYNMANNIENYDNKVANLTV 175
DB 224 TRQTVIIQLEKQLNRATT--NNSVLQKQLE-LMDTVHNLNL----- 264
QY 176 VVNSLDGKCSK---CPQSEHQSPVQVHLKYKDCSDHYVLGRSSGAYRVTDPHRNSSF 231
DB 265 -----CTREGVLLKGGKREEEP-----FRDCADYVQAGFNKSGIYTIYINMPEPK 311
QY 232 EYCDMETMGGWTVLQARLDGSGTNFTREWKDYKAGFNLREFEWLGNDKIHLLTSKEM 291
DB 312 KVCNMDVNGGWTVIQHRDEGSLDFQGWKEYKMGFGNPSGEYWLGNFEFPAITSQRY 371
QY 292 ILRIDLEFNGLTLYALYDQFYVANEFLKYLRIHIGNYNGTAGDALRFRSHYHNDLRFETT 351
DB 372 MLRIELMDWEGNRAYSQYDRHIGNEKQNYRLYKAGHTGTACKQSSLLILH-GAD---EST 427
QY 352 PDNDRYPSGNCGLYSSGWWFDSCLSANLNGKYYHQ-KYGVNRNGIFWGTWPGINAO 410
DB 428 KDADNDNCMC-KCALMLTGGWFDACGPSNLNGMEFYTAGQNHGKLNGLKWHYFKGPSY-- 484
QY 411 PGYKSSPKQAAMIRPKNF 430
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:04 ; Search time 21.07 Seconds
(without alignments)
368.175 Million cell updates/sec

Title: US-09-442-143-4
Perfect score: 2340
Sequence: 1 MRLPGWLWSSAVLAACRAV.....GYKSSFKQAKMMIRPKFKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2.6/prodata/2/iaa/5b_COMB.pep.*
3: /cgn2.6/prodata/2/iaa/6_COMB.pep.*
4: /cgn2.6/prodata/2/iaa/PCFUS_COMB.pep.*
5: /cgn2.6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	533.5	22.8	314	1	US-08-525-505A-2
2	533.5	22.8	496	1	US-08-373-579-6
3	533.5	22.8	496	2	US-08-418-595-6
4	533.5	22.8	496	2	US-08-665-926-6
5	533.5	22.8	496	3	US-09-162-437-6
6	524	22.4	312	1	US-08-525-505A-4
7	509	21.8	286	3	US-08-960-507-20
8	507	21.7	346	3	US-08-960-507-19
9	489.5	20.9	497	1	US-08-373-579-4
10	489.5	20.9	497	2	US-08-418-595-4
11	489.5	20.9	497	2	US-08-665-926-4
12	489.5	20.9	497	2	US-08-348-492-4
13	489.5	20.9	497	3	US-09-162-437-4
14	488.5	20.9	453	1	US-08-206-176-6
15	488	20.9	491	3	US-08-933-821-4
16	488	20.9	491	3	US-08-960-507-4
17	483.5	20.7	493	2	US-08-933-821-2
18	483.5	20.7	493	3	US-08-960-507-2
19	483	20.6	498	1	US-08-373-579-2
20	483	20.6	498	2	US-08-418-595-2
21	483	20.6	498	2	US-08-665-926-2
22	483	20.6	498	2	US-08-348-492-2
23	483	20.6	498	3	US-09-162-437-2
24	480.5	20.5	411	1	US-08-232-532-1
25	480.5	20.5	411	2	US-08-748-150-1
26	480.5	20.5	411	4	PCT-US95-05168-1
27	471.5	20.1	509	2	US-08-665-926-8
28	465.5	19.9	454	3	US-08-434-099A-27

29	465.5	19.9	454	3	US-08-434-099A-28	Sequence 28, Appl
30	463.5	19.8	282	3	US-08-812-586-49	Sequence 49, Appl
31	463	19.8	491	1	US-08-206-176-4	Sequence 4, Appl
32	454.5	19.4	470	2	US-08-933-821-6	Sequence 6, Appl
33	454.5	19.4	470	3	US-08-960-507-6	Sequence 6, Appl
34	452.5	19.3	1358	1	US-08-404-685-4	Sequence 4, Appl
35	452.5	19.3	1358	1	US-08-404-671-4	Sequence 4, Appl
36	452.5	19.3	1358	1	US-08-404-781-4	Sequence 4, Appl
37	444	19.0	214	3	US-08-960-507-21	Sequence 21, Appl
38	442.5	18.9	236	3	US-08-886-269-3	Sequence 3, Appl
39	442.5	18.9	236	3	US-09-167-647-4	Sequence 4, Appl
40	440.5	18.8	236	3	US-08-886-269-1	Sequence 1, Appl
41	440.5	18.8	236	3	US-08-886-269-2	Sequence 2, Appl
42	440.5	18.8	236	3	US-09-167-647-1	Sequence 1, Appl
43	440.5	18.8	236	3	US-09-167-647-2	Sequence 2, Appl
44	437.5	18.7	236	3	US-08-886-269-4	Sequence 4, Appl
45	437.5	18.7	236	3	US-09-167-647-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-525-505A-2
; Sequence 2, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAKO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-505A-2

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Query Match 22.8%; Score 533.5; DB 1; Length 314;
Best Local Similarity 38.28; Pred. No. 1.8e-43;
Matches 129; Conservative 46; Mismatches 103; Indels 53; Gaps 11;

QY 119 EDSRVQE---LESQVKNLSSELKNAKDQIOGLOGRLTILHLVNMNMIENIYVDNKVANLTV 175
Db 25 DENCLOEQVRLRAQVROLETRVKKQOVVIAQLLHEKE-VQFLDRGOEDSFID----- 75

QY 176 VVNSLDGKCKCPSQEHMQSQPVQHLLIYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVYC 235
Db 76 ----LGGK-----RH--YADCSEIYNDGFKHSGFYKIKPLQSLAEFSVYC 114

QY 236 DMETMGCGTVALOARLDGSTNFTREWKDYKAGFGNLER---EFWLGNDKIHLLITKSKEMI 292
Db 115 DMSD-GGGWTVIQRSDSENFRNWDYENGFGVOSNGEYWLGNKNINLLTMOGQDYT 173

QY 293 LRIDLEDNGLTLVLYDQFYVANEFLKRYLHIGNYNGTAGDALRFSRH-----YNHDL 346
Db 174 LKIDLTDEKNSRFAQYKFKVGDEKSEYELNIGYSGTAGDSLSGTFFPEVQWASHOT 233

QY 347 RFFTPDRDNDYPSGNGCLYSSGWFDSCLSANLKYHOKYKG-VRNGIFWGTWPG 405
Db 234 MKFSTRDNDNY-NGNCAEEQSGWFWNRCHSANLNGVYQGYRAETDNGVWVWTW-- 290

QY 406 INQAPGGYKSSFKQAKMMIRPKNKP 432
Db 291 -----RGWYSLKSVVMKIRPSDFIP 311

RESULT 2
US-08-373-579-6
; Sequence 6, Application US/08373579
; Patent No. 5650490
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
```

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-373-579-6

Query Match 22.8%; Score 533.5; DB 1; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CEGSQCPF-----QLFLPTLIOLPOLGSMEEVLKE-----VRTLKPAV-DSLUKKSQDC 97
Db 53 CRSSSPYVSNAVQADAPLEYDDSVQRLQVLEINMENTQWLKLENYIQDNMKKEV 112

QY 98 KLOADPHR-----DPGGNGNGAETAEDSR-VQLESOV-----NKL 133
Db 113 QQNAVQNTAVMTIEGTNLLN--OTAEQTRKLTDEVAQVNLNQTRLEQLLHLSLSTNKL 170

QY 134 SSELKNAKDQIOGLOGR-----LETLHLVNMNMIENIYVDN---KVANLTVVYVNSL 180
Db 171 EKQILDOTSEINKLQDNKSFLEKKVLAMEDKHIIQLOSIKEEKDQLOLVLYSKNSIIEEL 230

QY 181 DGKC-----SKPQSEHMQSQPVQHLLI-----YKDCSDHYVL 212
Db 231 EKKIVTATVNSVLQKQOQHDLMETVNNLLTMTSTNSAKDPTVAKERQISFRDCAEVFKS 290

QY 213 GRSSGAYRVTPDHRNSSFEVYCDMETMGGTVVQLARLDGSTNFTREWKDYKAGFGNLE 272
Db 291 GHTNGIYTLTFPNSSTEEIKAYCDMEAGGGGTIIQRRDGDGSDVDFQRTWKYKVGFGNPS 350

QY 273 REFWLGNDKIHLTLTKSKEMILRIDLEFNGLTLVLYDQFYVANEFLKRYLHIGNYNGTA 332
Db 351 GEVWLNKNEFVSQLTNQORYVVKILHLDKWEANEAYSLYEHFYLSEELNYRIHLKGLTGT 410

QY 333 GDALRFSRHYNHDLRFFTPDRDNDRYPSGNGCLYSSGWFDSCLSANLKYHOKYK 392
Db 411 GKISSISQPCND---FSTKDGNDKIC-KCSQMLTGGWFWFACGSPNLNGMYYPQRN 465

QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNF 430
Db 466 TNKFNGIKWYWKG-----SGY--SLKATMTMIRPADF 496

RESULT 3
US-08-418-595-6
; Sequence 6, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
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FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-6

Query Match 22.8%; Score 533.5; DB 2; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CEGSQCPE-----QLTPTLTITQLPROLGSMEVLEK---VRLTKEAV-DSLKKSCDQC 97
DB 53 CRSSSPYVNAVQDAPLEYDDSVQRLQVLENNMTQWLKLENYIQDNMKKEMVEI 112
QY 98 KQADDDR-----DPGGNGGNGAETAEDSR-VOELESQV-----NKL 133
DB 113 QONAVQNOTAVMIEIGTNLLN--QTAEQTRKLTDEVAQVLTQTTREQLLLEHSLSTNKL 170
QY 134 SSELKNKDOIQLOGR-----LETLHVNMMNIENYVDN---KVANLTVVVSNSL 180
DB 171 EKQILDOTSEINKLQDNKSFLEKVKVLAMEDKHIIQLOSIKEEKDQLQVLSKQNSIEEL 230
QY 181 DGKC-----SKCPSQPHMQSQPVQHLI-----YKDCSDHYVL 212
DB 231 EKKIVTATVNVSVLQKQOQDLMTETVNNLLTMMSTNSAKDPTVAKKEQISFRDCAEVFKS 290
QY 213 GRSSGAYRVTPDHRNSSPEVYCDMETGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE 272
DB 291 GHTNGIYTLTPNSTEIEIKAYCDMEAGGGWTIIORREDGSDVDFQRTWKYKVGFGNPS 350
QY 273 REFVWGNKIHLLTKSKEMILRIDLEDFNGLTYALYDOFYVANEFKYLRLHIGNYNGTA 332
DB 351 GEYWLGNFVSQLTNQORYVLKHLKDWEGNEAYSLEYEHFVLSSEELNYRIHLKGLTGTA 410
QY 333 GDALRFSRHYNDLRFPTTDRDNDRYPSGNCGLIYSSGWWFSDCLSANLNGKYYHQYK 392
DB 411 GKISSIQPND-----FSTKGDNDKIC-KCSQMLTGWGWFSDACGPNLNGMYTPQRN 465
QY 393 GVR-NGIFWGTWPGINQAOPGGYKSSFKQAKMIRPKNF 430
DB 466 TNKFNKIKWYKKG-----SGY--SLKATYMMIRPADF 496

RESULT 4
US-08-665-926-6
Sequence 6, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-6

Query Match 22.8%; Score 533.5; DB 2; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CEGSQCPE-----QLTPTLTITQLPROLGSMEVLEK---VRLTKEAV-DSLKKSCDQC 97
DB 53 CRSSSPYVNAVQDAPLEYDDSVQRLQVLENNMTQWLKLENYIQDNMKKEMVEI 112
QY 98 KQADDDR-----DPGGNGGNGAETAEDSR-VOELESQV-----NKL 133
DB 113 QONAVQNOTAVMIEIGTNLLN--QTAEQTRKLTDEVAQVLTQTTREQLLLEHSLSTNKL 170
QY 134 SSELKNKDOIQLOGR-----LETLHVNMMNIENYVDN---KVANLTVVVSNSL 180
DB 171 EKQILDOTSEINKLQDNKSFLEKVKVLAMEDKHIIQLOSIKEEKDQLQVLSKQNSIEEL 230
QY 181 DGKC-----SKCPSQPHMQSQPVQHLI-----YKDCSDHYVL 212
DB 231 EKKIVTATVNVSVLQKQOQDLMTETVNNLLTMMSTNSAKDPTVAKKEQISFRDCAEVFKS 290
QY 213 GRSSGAYRVTPDHRNSSPEVYCDMETGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE 272
DB 291 GHTNGIYTLTPNSTEIEIKAYCDMEAGGGWTIIORREDGSDVDFQRTWKYKVGFGNPS 350
QY 273 REFVWGNKIHLLTKSKEMILRIDLEDFNGLTYALYDOFYVANEFKYLRLHIGNYNGTA 332
DB 351 GEYWLGNFVSQLTNQORYVLKHLKDWEGNEAYSLEYEHFVLSSEELNYRIHLKGLTGTA 410
QY 333 GDALRFSRHYNDLRFPTTDRDNDRYPSGNCGLIYSSGWWFSDCLSANLNGKYYHQYK 392
DB 411 GKISSIQPND-----FSTKGDNDKIC-KCSQMLTGWGWFSDACGPNLNGMYTPQRN 465
QY 393 GVR-NGIFWGTWPGINQAOPGGYKSSFKQAKMIRPKNF 430
DB 466 TNKFNKIKWYKKG-----SGY--SLKATYMMIRPADF 496

RESULT 5
US-09-162-437-6
Sequence 6, Application US/09162437

Db 265 -----CTKEVLLKGGKREDEK-----PRDCADYVQAGFNKSGIYTIYINWPEPKK 311
Qy 233 VYCDMETGGGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSKEMI 292
Db 312 VFCNMDVNGGWTVIQIHREDGSLDFQGWKEYKMGFGNPGSEYWLGNFIFAITSQRYM 371
Qy 293 LRTDLEDFNGLTYALYDQYVANEFLKYLRLHIGNYNGTAGDALRFRSRHYNDLRFETTP 352
Db 372 LRIELMDWEGNRAYSQYDRFHIGNEKQNYRLKLGHTGTAGKQSSLIH-GAD---FSTK 427
Qy 353 DRNDRYPGNCGLYSSGWMFSCLSANLNGKYYHQ-KYKGVENGFWGTWPGINQAO 411
Db 428 DADNDNMC-KCALMTGTGWMFSCLSANLNGKYYHQ-KYKGVENGFWGTWPGINQAO 411
Qy 412 GYGKSSFKQAKMIRPKNF 430
Db 484 -----SLRSTTMMIRPLDF 497
RESULT 14
US-08-206-176-6
; Sequence 6, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Dalrymple, Michael A
; APPLICANT: Prunkard, Donna E
; APPLICANT: Foster, Donald C
; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,176
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-176-6

Query Match 20.9%; Score 488.5; DB 1; Length 453;
Best Local Similarity 32.9%; Pred. No. 7.1e-39;
Matches 136; Conservative 54; Mismatches 152; Indels 71; Gaps 18;
Qy 50 GSCQPFQL-----TLPLTTLQPLQGLSMEEVLKVRTLKEAVDSLKSCQDCKLQADHR 105
Db 42 GSYCTPTCGIADPLSTYQTKVDRDLQASLEDILHQVENKTSVKQLIKAIQ-LATYNPDSS 100
Qy 106 DPGNGNGNGAETAE-DSRVOELESQVKNLSSELKNAKDQIQGLQGRLETLHLVNMNEN 164

Db 101 KP-----NMIDAATLKSRP--MLEIMKYEASILTHDSSIRYLQ-----EYNSNN--- 144
Qy 165 YVDNKVANLTVVNSLDGKSCPCSQEHMQSQPVQHLIYKDCSDHYVLGRRSSGAYRVTP 224
Db 145 ---QKIVNLKKEVAQLEAQCQE-PCKDVTQ---IHDITKDCQDITANKAKOSGLYFIKP 197
Qy 225 DHRNSSFEYVCDMETGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE-----REFWLGND 280
Db 198 LKANQOQLVYCEIDGSGNGWTFQKRLDGSVDFKKNWIOYKEGFGHLSPTGTTEFWLGNE 257
Qy 281 KIHLLTKSKEM--ILRIDLEDFNGLTYALYDQYVANEFLKYLRLHIGNY-NGTAGDAL- 336
Db 258 KIHLLISTOAIYALYALVELEDNGRTSTADYAMFKYGPEDAKYRLTYAYFAGGDAGDAFD 317
Qy 337 -----REFSRHYNHDLREFTTPDRNDRYPGNCGLYSSGWMFSCLSANLNGKY 386
Db 318 GFDFGDDPSDKF--FTSHNGMQFSTWDNDNDF-EGNCAEQDQSGWMMKCHAGHLNGYV 374
Qy 387 YH-----QYKGYVRNGIFWGTWPGINQAOPEGYSK---SFKQAKMMIRPKN 429
Db 375 YQGGTYSKASTPGYDNGIWIATW-----KTRWYSMKKTKTKIIPFN 416
RESULT 15
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-4

Query Match 20.9%; Score 488; DB 2; Length 491;
Best Local Similarity 27.0%; Pred. No. 9.1e-39;
Matches 129; Conservative 80; Mismatches 143; Indels 126; Gaps 15;
Qy 46 GRCEGSCQPFQLTLPPLTIQLP-----RQLGSMEEVL-----KEVFT 82
Db 42 GKAEAKKCAVFLVPEQRITGTCVNTKQDASTIKDMITRMDLENLKDVLRSQKREIDV 101
Qy 83 LKEAVDSLKSCQDCKLQADHRDPGGNGNGCAETAEADSRVOELESQVKNLSSELKNAKD 142

Db 102 LOLVVDVGNIVNEVKLLRKSRN-----MNSRVTQLYMQ---LLHEIIRKRD 146
Qy 143 ---OIOGLOGRL--ETLHLVNNNNIENYVDKNVANITVVVNS-----LDGKCSKCP SQ 190
Db 147 NSLELSQLENKILNVVTETMLKMATRYRELEVKYASLTDLVNNSQSVMITLLEEQCLRFSR 206
Qy 191 EHMOSQP-----VQHL----- 201
Db 207 QDTHVSPPLVQVVPQHIPNSQQYTPGLLCGNEIQDPGYPRDLMPPDPLATSPTKSPFKI 266
Qy 202 -----IYKDCSDHYVLGRSSGAYRTPDHRNSSFEVYCDMETMGGGWTVLQARLD 252
Db 267 PPVTEINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPWLNCENSILDPGGWTVIOKRTD 326
Qy 253 GSTNTRWKDYKAGFNLEREFWLCNDKIHLLITKSKEMILRIDLEDFNGLTLYALYDQF 312
Db 327 GSVNFRWNENYKKGFGNIDGEYWLGLENIYMLSNODNYKLLIELEDWSDKKVYAEYSSF 386
Qy 313 YVANEFLKYLHIGNYNGTAGDALRESRHYNHDRLREFTTPDRDNDRYPSGNCGLYYSSGW 372
Db 387 RLEPESEYRLRLGTYQGAGDSMMW-----HNGKQFTTLDKDKMY-AGNCAHFHKGGW 440
Qy 373 WFDCLSANLNGYY---HOKYKGVNRNGIFWGTWPGINQAQPGYKSSFKQAKMMIRP 427
Db 441 WYNACAHSNLNGVWYRGGHYRSKH-QDGIFWAEYRG-----GSY--SLRAVQMMIRP 489

Search completed: February 27, 2001, 12:48:06
Job time: 32 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:35 ; Search time 53.35 Seconds
(without alignments)
964.466 Million cell updates/sec

Title: US-09-442-143-2
Perfect score: 2378
Sequence: 1 MKLANWYLLSSAVLATYGFLL.....GYKSPFKKMMIRPKHKFP 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL15:*
- 1: sp-archaea:*
 - 2: sp-bacteria:*
 - 3: sp-fungi:*
 - 4: sp-human:*
 - 5: sp-invertebrate:*
 - 6: sp-mammal:*
 - 7: sp-mhc:*
 - 8: sp-organelle:*
 - 9: sp-phage:*
 - 10: sp-plant:*
 - 11: sp-rodent:*
 - 12: sp-virus:*
 - 13: sp-vertebrate:*
 - 14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2378	100.0	439	4	Q14314	Q14314 homo sapien
2	618.5	26.0	652	5	Q5ND01	Q9ndq1 ciona intes
3	525	22.1	496	11	Q35608	Q35608 mus musculu
4	524.5	22.1	375	6	Q77802	Q77802 bos taurus
5	523.5	22.0	495	4	Q9P2Y7	Q9P2Y7 homo sapien
6	523	22.0	407	13	Q9PU54	Q9pu54 gallus gall
7	522	22.0	496	4	Q15123	Q15123 homo sapien
8	520	21.9	444	4	Q9NR87	Q9nr87 homo sapien
9	506.5	21.3	312	4	Q98830	Q98830 homo sapien
10	505	21.2	491	4	Q95841	Q95841 homo sapien
11	489	20.6	346	4	Q43827	Q43827 homo sapien
12	486.5	20.5	498	4	Q15389	Q15389 homo sapien
13	485.5	20.4	292	5	Q9U8W8	Q9u8w8 tachypleus
14	485.5	20.4	493	11	Q9R045	Q9r045 mus musculu
15	483.5	20.3	498	11	Q08538	Q08538 mus musculu
16	482.5	20.3	488	13	Q91589	Q91589 xenopus lae
17	481.5	20.2	493	11	Q9J303	Q9j303 rattus norv
18	480.5	20.2	493	4	Q9UKU9	Q9uku9 homo sapien
19	476	20.0	308	5	Q9U8W6	Q9u8w6 tachypleus

20	475	20.0	435	13	Q93568	Q93568 gallus gall
21	471	19.8	316	5	Q9U8W7	Q9u8w7 tachypleus
22	470.5	19.8	509	11	Q9WVH6	Q9wvh6 mus musculu
23	467	19.6	481	6	Q18920	Q18920 bos taurus
24	462	19.0	334	11	Q70165	Q70165 mus musculu
25	450	18.9	503	4	Q9Y264	Q9y264 homo sapien
26	438.5	18.4	335	11	Q9WTS8	Q9wts8 rattus norv
27	435.5	18.3	235	6	Q28763	Q28763 papio hamad
28	434.5	18.3	326	6	Q29042	Q29042 sus scrofa
29	428.5	18.0	323	6	Q29041	Q29041 sus scrofa
30	427	18.0	316	6	Q28529	Q28529 mustela put
31	427	18.0	319	4	Q92596	Q92596 homo sapien
32	423	17.8	326	4	Q00602	Q00602 homo sapien
33	423	17.8	1353	13	Q00546	Q00546 gallus gall
34	421.5	17.7	306	11	Q70497	Q70497 mus musculu
35	421	17.7	712	4	Q00531	Q00531 homo sapien
36	421	17.7	1358	4	Q92752	Q92752 homo sapien
37	421	17.7	1358	4	Q15568	Q15568 homo sapien
38	420.5	17.7	307	6	Q28703	Q28703 oryctolagus
39	420	17.7	313	4	Q15485	Q15485 homo sapien
40	417.5	17.6	1356	11	Q05546	Q05546 rattus norv
41	414.5	17.4	299	4	Q75636	Q75636 homo sapien
42	412.5	17.3	387	5	Q18546	Q18546 biophalari
43	405	17.0	440	5	Q9W291	Q9w291 drosophila
44	403.5	17.0	220	6	Q02411	Q02411 sus scrofa
45	403.5	17.0	417	6	Q29038	Q29038 sus scrofa

ALIGNMENTS

RESULT 1
ID Q14314 PRELIMINARY; PRT; 439 AA.
AC Q14314;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytela R.
RT "Sequence of a human transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1995).

RA YUWARAJ S., LIU M., MARSDEN P., LEVY G.;
RT "Cloning and characterization of Hfg12: The human counterpart to the
RT mouse gene Egl2.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z36531; CAA85298.1; .
DR EMBL; AF104015; AAD10825.1; .
DR EMBL; AF104014; AAD10825.1; JOINED.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; .
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 439 AA; 50228 MW; DF34656288B49B68 CRC64;

Query Match 100.0%; Score 2378; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 1e-149;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLANWYLLSSAVLATYGFLLVANNTEELKDERAKDVCVRLESRCCKCEAGCPQVQS 60
|||||


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Db 304 NSTEIKAYCDMDVGGGWTVIQHRDEGSDVDFQRTWKYKEGFGNPLGEGYWLGNFEVSOL 363
QY 293 TKSEMIILRIDLEDPNGVELYALYDOFYVANEFLKYLHVGNNGTAGDALRNFKNHND 352
Db 364 TGOHYVLKIQKDWEGNEANSLYDHFYLAGEESYRHLTGLTGTAAKISSISQPSGD- 422
QY 353 LKFTTPDKNDRYPSGNGLYSSGWFWDACLSANLNGKYHQYRGVR-NGIFWTWP 411
Db 423 --FSTKSDNDKIC-KCSQMLSGWGFWDACGPNLNGQYYPQKONTKNGIKWYWK 478
QY 412 GYSAHPCGYKSSPKKAKMIRPKHF 437
Db 479 G-----SGY--SLKATTMMIRPADF 496

RESULT 4
O77802 PRELIMINARY; PRT; 375 AA.
AC O77802; Q9TSK0;
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 (FRAGMENT).
GN ANGPT2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394 (1998).
RN [2]
RP SEQUENCE OF 219-355 FROM N.A.
RC TISSUE=ADRENAL CORTEX;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859 (1998).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS
CC FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC
CC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX
CC CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT
CC VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE
CC ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
CC PERMISSIVE ANGIOGENIC SIGNAL.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE. OVEREXPRESSED DURING LUTEOLYSIS. THIS COULD REFLECT THE
CC REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
CC THE MIDSTAGE CORPUS LUTEUM.
CC -1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL: AF094599; AAC62490.1; -.
DR EMBL: AF032924; AAC78285.1; -.
DR HSSP: P02671; IFZD.
DR INTERPRO: IPR002181; -.
DR PFAM: PF00147; fibrinogen_C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON_TER
FT CONFLICT 272 272 S -> L (IN REF. 2).
SQ SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

Query Match 22.1%; Score 524.5; DB 6; Length 375;
Best Local Similarity 34.2%; Pred. No. 3e-27;

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Matches 136; Conservative 58; Mismatches 139; Indels 65; Gaps 14;
QY 61 LPPLTIQLPKQFSRIEVEFQVNLKEIV--NSLKSCQD-----CKLOADDNGDGPGRNG 113
Db 22 LTDVEAQVNLQTTFL-----ELQLLEHSLSTNKLKLEKILDOITSEISKLO-----DKNS 69
QY 114 LLPSTGAPGEVDNRVRELESEVKNLSSELKNAKEEINVLHGR-----LEK-LNLVN 165
Db 70 FL-----EKKVLDMEDKHIVQLRSIKEKQDLQVLVSKNSIIEELEKQLVTAT 118
QY 166 MNNI-----ENYVDSKVANLTFVNSLDGKCKSPQEOIQSRPVQHLIVKDCSDYIAG 220
Db 119 VNNSVLQKQOQHDLMETVNNLLTLMSTSNPSYSLAKDEQI-----IFRDCGEAFKSG 170
QY 221 KRSEYRVTPDPKNSFEVYCDMETMGGWTVLQARLDGDTNFTRTWODYKAGFGRLR 280
Db 171 LTTSGYVTLTFPNSTEEIKAYCDMETGGGWTVIQRDEGSDVDFQRTWKYKVGFGNPSG 230
QY 281 EFWLGNKDHIHLTKSEMILRIDLEDPNGVELYALYDOFYVANEFLKYLHVGNNGTAG 340
Db 231 EHLGNEFVSQVTGQKRYVLKIHLDWEGNEAYSLYDHFYLSNEELNYRIHLKGLTGTAG 290
QY 341 DALRFNKHYNHDLKFTTPDKNDRYPSGNGCLYSSGWFWDACLSANLNGKYHQYRG 400
Db 291 KISSISQPGND----FSTKADNDKIC-KCSQMLTGGWGFWDACGPNLNGMYYPQONT 345
QY 401 VR-NGIFWTWPVCGVSEAHPCGYKSSPKKAKMIRPKHF 437
Db 346 NKFNIGIKWYWKG-----SGY--SLKATTMMIRPADF 375

RESULT 5
Q9P2Y7 PRELIMINARY; PRT; 495 AA.
AC Q9P2Y7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA Wands J.R.;
RT "Biologic significance of angiotensin-2 expression in human
RT hepatocellular carcinoma.";
RL J. Clin. Invest. 103:341-345 (1999).
DR EMBL: AB009865; BAA95590.1; -.
SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;

Query Match 22.0%; Score 523.5; DB 4; Length 495;
Best Local Similarity 28.1%; Pred. No. 5e-27;
Matches 139; Conservative 76; Mismatches 155; Indels 125; Gaps 16;
QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFQVQN 84
Db 26 MDSIGKKQYQVHGSCSYTFLLPEDMNCRSSSPYVSNVQORDAPLEYDDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQDCKLOADDNGDGPGRNGLLLPSTGAPGEVDN---- 128
Db 86 IMENNTQWLKLENYIQDNMKKEWETIQNAVQN-----QTAVMIEICTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR-----LEKL 161
Db 135 TABQTRKLTDEVAQVNLQTTFLQLLEHSLSTNKLKLEKILDOITSEINKLQDNKSLERK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIEEKDQQLVLYSKNSIIEELEKKIVTATVNNVSLQKQOHDLMET 254

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Db 195 VLAMEKDHIIQLOSKEEKDQLOVLVSKNSIIIEELEKKIVTATVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKSCSPQEQOIRPVQHLIYKDCSDYAIAGKRSSETRYTPDPKNSSEFYVCD 243
Db 255 VNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTNGIYTLTFPNSTEIKAYCD 314
Qy 244 METMGGWTVLQARLDGSTNFTWQDYKAGFGLNRREFWLGNKDKIHLTKSKEMILRID 303
Db 315 MEAGGGWTTIQRREDGSDVDFORTWKEYKVGFGNPGSEYWLGNFVSLQTNQOQRYVLKI 374
Qy 304 LEDFNGVELYALYDOFYVANEFLKVLHVGNYNGTAGDALRNFKNHNDLKFETTPDKON 363
Db 375 LKDWEGNEAYSLEYHFYLSSEELNRYHLGLGTGAKTSSISQPGND---FSTKGDGN 430
Qy 364 DRYPGNGCLYSSGWWFADCLSANLNGKYYHOKYRGVR-NGTFWGTWPGVSEAHPCGYK 422
Db 431 DXCIC-KCSQMTGGWFDACGPNLNGMYYPQONTNFKNGIKWYWG------SGY- 482
Qy 423 SSFKEAKMMIRPKHF 437
Db 483 -SLKATTMMIRPADF 496

RESULT 8
Q9NR7 PRELIMINARY; PRT; 444 AA.
AC Q9NR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 ISOFORM-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
human angiotensin-2."
RL J. Biol. Chem. 275:18550-18556(2000).
DR EMBL; AF187858; AAF76526.1; -.
SQ SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;

Query Match 21.9%; Score 520; DB 4; Length 444;
Best Local Similarity 29.6%; Pred. No. 7.4e-27;
Matches 134; Conservative 74; Mismatches 154; Indels 90; Gaps 15;
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Qy 43 LESRGKCE---EAGCPCYQVSLPPL---TIOLPKQFSRIE-----EVFKVQNLKEIVN 90
Db 26 MDSIGKQYQVQHGSCSTFLPEMDNCRSSSPYVSNVAVQDAPLEYDDSVQRLQVLEN 85
Qy 91 SLKSC-----QDCKLQADDGDPGRNGLLPLSTGAPGEVGNRVRELESEVKNLSS 142
Db 86 IMENNTQMLKVLNQTRELEQ-----LLEHSLSTNKL-EKQILDQTSINKLQD 134
Qy 143 -----ELKNAKEEINVHGRLEKLNLVNMMNIENYVDSKVAN----- 179
Db 135 KNSFLEKKVLAMEDKHIIQLOKSEKQDQVLVSKNSI-IEELEKKIVTATVNNSVLQ 193
Qy 180 -----LTFVNSLDGKSCSPQEQOIRPVQHLIYKDCSDYAIAGKRSSET 226
Db 194 KOQHDLMETVNNLLTMMSTNSAKDPTVAKEEQIS-----FRDCAEVFKSGHTNGI 245
Qy 227 YRVTPDPKNSSEFYVCDMETMGGWTVLQARLDGSTNFTWQDYKAGFGLNRREFWLGN 286
Db 246 YTLFPNSTEETKAYCDMEAGGGWTTIQRREDGSDVDFORTWKEYKVGFGNPGSEYWLGN 305
Qy 287 DKIHLLTKSKEMILRIDLEDFNGVELYALYDOFYVANEFLKVLHVGNYNGTAGDALRNF 346
Db 306 EFVSQLTNQORYVLKHLKDWEGNEAYSLEYHFYLSSEELNRYHLKGLGTGAKTSSIS 365
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Qy 347 KYNHNDLKFETTPDKNDRYPSGNGCLYSSGWWFADCLSANLNGKYYHOKYRGVR-NGI 405
Db 366 QPGND-----ESTKGDNDKIC-KCSQMTGGWFDACGPNLNGMYYPQONTNFKNGI 420
Qy 406 FWGTWPGVSEAHPCGYKSSFKKAKMMIRPKHF 437
Db 421 KWIYWG-----SGY--SLKATTMMIRPADF 444

RESULT 9
Q08830 PRELIMINARY; PRT; 312 AA.
AC Q08830;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR.
GN HFREP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOMA;
RC MEDLINE=93290661; PubMed=8390249;
RA Yamanoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
related gene, HFREP-1."
RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
CC -!- TISSUE SPECIFICITY: OVEREXPRESSED IN HEPATOCELLULAR CARCINOMAS.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL; D14446; BAA03336.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Plasma; Blood coagulation; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 312 FIBRINOGEN-LIKE PROTEIN 1.
FT SIMILAR 70 296 BETA/GAMMA CHAINS OF FIBRINOGEN.
FT DISULFID 83 112 BY SIMILARITY.
FT DISULFID 248 261 BY SIMILARITY.
SQ SEQUENCE 312 AA; 36378 MW; 2330F3D60CD0BBA8 CRC64;
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Query Match 21.3%; Score 506.5; DB 4; Length 312;
Best Local Similarity 36.8%; Pred. No. 3.7e-26;
Matches 118; Conservative 38; Mismatches 108; Indels 57; Gaps 9;

Qy 129 RVRELESEVKNLSSELKNAKEEINVHGRLEKLNLVNMMNIENYVDSKVANLTFVNSLD 188
Db 36 QVRLLETRVQOQVKIKQLQE-----NEVQFLQGDDETVVD----- 73
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Qy 189 GKSCSPQEQOIRPVQHLIYKDCSDYAIAGKRSSETRYTPDPKNSSEFYVCDMETMG 248
Db 74 -----LGSKRQ-----YADCSIFNDGYKLSGFIKPLQSPAESFYVCDMSD-G 117
Qy 249 GGWTVLQARLDGSTNFTWQDYKAGFGLNRREFWLGNKDKIHLTKSKEMILRIDLE 305
Db 118 GGWTVLQARRSDGSENFNRGKWDYENGFGNFVQKHGEYWLGNKLNHFLTQEDYTLKIDLA 177
Qy 306 DFNGVELYALYDOFYVANEFLKVLHVGNYNGTAGDALRNFKNH-----YNHDLKFETTP 359
Db 178 DFEKNSRYAQYKFKVGDENKFNELNGEYSGTAGGDSLAGNFHPEVQWASHQRMKESTW 237
Qy 360 DKDNDRYPSGNGCLYSSGWWFADCLSANLNGKYYHOKYRG-VRNGIFWGTWPGVSEAH 418
Db 238 DRDHNY-EGNCAEEDSGWFWNFRCHSANLNGVYISPGYPTAKTDNGIVWYTW----- 288
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QY 419 GGYKSSFKKAKMMIRPKHKFP 439
Db 289 HGWWYSLKSVVMKIRPNDFIP 309

RESULT 10
ID 095841 PRELIMINARY; PRT; 491 AA.
AC 095841;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ANGIOPOIETIN Y1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiotensin family
protein, angiotensin-3".
RL FEBS Lett. 443:353-356(1999).
DR EMBL; AF107253; AAD19608.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen.C.1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 491 AA; 56719 MW; 3C4DB8DEF6CF7E99 CRC64;

Query Match 21.2%; Score 505; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 8.3e-26;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;
QY 47 GKCEAGCEPYQVSLPPLTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
Db 42 GK-EAKKCACTELVPEQRITGPICVTKGQDASTIKDMITRMDLENLKDVLRSQKREID 100
QY 98 DCKLQADDNGDGRGNGLLLPSTGAPGEVGNRVRELSEVKNLSKLNKAEENLVHGR 157
Db 101 VLQLVVDVDGN-----IVNEVKLLKRESNMNSMRTVQLYMQ 136
QY 158 L-----EKLNLVNMNNIENV-----DSKVANLTPVNS-----L 187
Db 137 LHEIITRKDNLSOLENKLNTVTEMLKMATRYRELEVKYASLTDLVNNQSVMITLL 196
QY 188 DGKCSKCPSEQIQSRP-----VQHL----- 208
Db 197 EEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQOYTPGLLGNGEIQRDPCYPRDLMPDPA 256
QY 209 -----IYKDCSDYYAIGKRSSEYRVTPDPKNSFFVYCDMETWGG 249
Db 257 TSPTKSPFKIPPTFFINEGPFKDCQQAKEAGHSVSGIYMIKPENSGMPQLWCENSLDPG 316
QY 250 GWTVQARLDGNTFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMILRDLDEFG 309
Db 317 GWTVQKRTDGSVNFRRWENYKKGFGNIDGXYWLGLENIYMLSNQDNVYKLLIELEDWSD 376
QY 310 VELVYALYDQFYVANEFLKRLHVGNYNGTAGDALRFRNKHYNHDLKFFTPDKDNDRYPG 369
Db 377 KYVYAEVSSFRLEPESEFYRLRLGTQYOGNAGDSMMW-----HNGKQFTLDRDKDY-AG 430
QY 370 NCGLYSSGWNFDACLSANLNGKYYH--OKYRGV--RNLFWTWPQVSAHPGGYKSSPK 427
Db 431 NCAHFHKGWYNAACHASNGLNGVYRGCHYRSKHQDGLFWAEYRG-----GSY--SLRA 482
*QY 428 AKMWIRP 434
Db 483 VQMWIRP 489

RESULT 11
ID 043827 PRELIMINARY; PRT; 346 AA.
AC 043827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CDT6.
GN DJ647M16.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORNEA;
RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y16132; CAA76078.1; -.
DR EMBL; AL049653; CAB44734.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen.C.1.
SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;
Query Match 20.6%; Score 489; DB 4; Length 346;
Best Local Similarity 36.2%; Pred. No. 6.1e-25;
Matches 117; Conservative 55; Mismatches 113; Indels 38; Gaps 13;
QY 130 VRELSEVKNLSSEK--NAKEE---INVHGRLE-KLNLVNMNNIENVDSKVANLTFV 183
Db 49 VKELKAQVANLSLLSELNKKQERDWSVYVMQVMELESNKRMSRLTDAESKYSNMNQ 108
QY 184 VNSLDGCKSKCPSEQIQSRPVQHLIYKDCSDYYAIGKRSSEYRVTPDP--KNSSEFVY 241
Db 109 IDIMQLQAQVYQTSADA-----IY-DCSLYQKNYRISGVYKLPDDFLGSPLELVF 161
QY 242 CDMETGGGWTVLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMILR 301
Db 162 CDMETSGGGWTIIQRKSGLVSVFYRDWKYKQFGSIRGDFWLGNEHRLSQPTR-LR 220
QY 302 IDEDFNGVELYALYDQFYVANEFLKRLHVGNYNGTAG--DALRFRNKHYNHDLKFFTPD 360
Db 221 VEMEDWEGNLRVYAEYSHFVLGNELNSYRFLGNYTGNVGNDAQY-----HNNTAFSTKD 275
QY 361 KNDRYPSCNCGLYSSGWNFDACLSANLNGKYY-----HOKYRGVNRNGIFWGTWPGVSEA 416
Db 276 KDNDC-LDKAQLRKGQYNYNCCTDSNLNGVYRLGEHNKH---LDGITWYGMHGST-- 329
QY 417 HPGYKSSFKKAKMMIRPKHKFP 439
Db 330 -----YSLKRVEMKIRPEDFP 346
RESULT 12
ID Q15389 PRELIMINARY; PRT; 498 AA.
AC Q15389;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ANGIOPOIETIN-1 (ANG-1).
GN ANGPT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN	[1]	SEQUENCE FROM N.A.
RP		TISSUE=FETAL LUNG;
RC		MEDLINE-971134663; PubMed=8980223;
RX		Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA		Ryan T.E., Bruno J., Radziejewski C., Maisonnier P.C.,
RA		Iancopoulos G.B.;
RT		"Isolation of angiotensin-converting enzyme-related protein-1, a ligand for the TIE2 receptor, by
RT		secretion-trap expression cloning.";
RL		Cell 87:1161-1169(1996).
RN	[2]	
RP		SEQUENCE OF 307-498 FROM N.A.
RX		MEDLINE-96051387; PubMed=7584026;
RA		Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
RA		Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT		"Prediction of the coding sequences of unidentified human genes. I.
RT		The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT		analysis of randomly sampled cDNA clones from human immature myeloid
RT		cell line KG-1.";
RL		DNA Res. 1:27-35(1994).
RN	[3]	
RP		SEQUENCE OF 307-498 FROM N.A.
RX		MEDLINE-96051389; PubMed=7584028;
RA		Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
RA		Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT		"Prediction of the coding sequences of unidentified human genes. I.
RT		The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT		analysis of randomly sampled cDNA clones from human immature myeloid
RT		cell line KG-1 (supplement).";
RL		DNA Res. 1:47-56(1994).
CC	-1-	FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2
CC		TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC		PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC		CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC		ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC		VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC		HEART EARLY DEVELOPMENT.
CC	-1-	MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC		IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOCAL
CC		PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC		ISCHEMIC HEART.
CC	-1-	SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC		THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
CC	-1-	PTM: GLYCOSYLATED.
DR	EMBL:	U83508; AAA05057.1; -
DR	EMBL:	D13628; BAB02793.1; -
DR	HSP:	P02671; 1FZD.
DR	MM:	601667; -
DR	INTERPRO:	IPR002181; -
DR	PFAM:	PF00147; fibrinogen_C.1.
DR	PROSITE:	PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW	Glycoprotein:	Coiled coil.
FT	DOMAIN	81 119 COILED COIL (POTENTIAL).
FT	DOMAIN	153 261 COILED COIL (POTENTIAL).
FT	DOMAIN	284 498 FIBRINOGEN BETA/GAMMA.
FT	CARBOHYD	92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	498 AA; 57513 MW; 505FA63AEF6BE920 CRC64;
		Query Match 20.5%; Score 486.5; DB 4; Length 498;
		Best Local Similarity 32.3%; Pred.No.1.4e-24;
		Matches 131; Conservative 59; Mismatches 136; Indels 79; Gaps
QY	61	LPPLTLQLPKQSRIE-----EVFEVQNKLKEIVNSLKSCDCCKLOADNDGPGRN 112
Db	145	LTDVEVQLNQTSRLRIQLLENSLSLTYSKLEKQLLOQTNEILKIHE-----KN 191
QY	113	GLLLPSTGAPGEVDNRVRSELSVNKLSSELKNAKEINVLHG-----RLEK-L 161

Db 192 SLI-----EHKILEM-----GKHKBELDTLKEENLQGLVTRQTYITIQLEKQL 237
 Qy 162 NLVNNNNTIYVDSKVANLTFVNSLQKSK-----CPQOEIQSRPVQHLIYKDCSDY 217
 Db 238 NRATNN--SVLQKQLELMDTVHNLVNLCTKEGVLKGGKREKP-----FRDCADY 230
 Qy 218 AIGKRSSEYRV-----TPDPKNSFEYCYDMETMGGWTVLQARLDGSTNFTFTWODYKA 273
 Db 291 QAGFNKSGIYIYINNPEPK---KVFCDNVNNGGWTVIQHREDGSLDFQGWKEYKM 346
 Qy 274 GFGNLRREFWLGNDKIHLLTKSEMIILRIDLEDFNGVELYALYDQFYVANEFKYRLHVG 333
 Db 347 GFGNPSGEYLLWNEFIFAITSQRYMLRIELMOWEGRNAYSYDRFHIGNEKONYRLYK 406
 Qy 334 NYNCTAGDALRFNKHYNHLKFFTTDPKDNDYPSGNCGLIYSSGWWFADCLSANLNGY 393
 Db 407 GHTGTAGKQSSLIH-CAD---FSTKDADNDNCM-KCALMLTGGWWFADCGPSNLNGWF 461
 Qy 394 YHO-KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKKAMIRPKHF 437
 Db 462 YTAGQNHGKLNGIKWHYFKGPS-----YSLRSTMTMIRPLDF 498

 RESULT 13
 Q9U8W8
 ID Q9U8W8 PRELIMINARY; PRT; 292 AA.
 AC Q9U8W8
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE TECHLECTIN-5A.
 OS Tachyplesus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 OC NCBI_TaxID=6853;
 [1]
 RP SEQUENCE FROM N.A.
 RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
 RA Mizuno Y., Wai S.N., Iwanaga S., Kawabata S.;
 RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
 RT immunity are structurally related to fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
 DR EMBL; AB024737; BAA84188.1; -.
 DR HSSP; P02671; 1FZD.
 DR INTERPRO; IPR002181; -.
 DR PFAM; Pf00147; fibrinogen.C; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;

 Query Match 20.4%; Score 485.5; DB 5; Length 292;
 Best Local Similarity 36.3%; Pred. No. 8.4e-25;
 Matches 106; Conservative 49; Mismatches 104; Indels 33; Gaps

 Qy 159 EKLNLVNMNNIYVDSKVANLTFVNSLDG-KCSKCPQOEIQ-----SRPVQHLIY 210
 Db 16 QKYGLTSSQNK-----LCDVTSSTGLDLSIKVMASHVKEQLKDKGTSEVAQPIVSPDP 69
 Qy 211 KDCSDIYAIGKRSEYRYVTPDP-KNSSEFYCDMETMGGWTVLQAR---LDGSTNFT 265
 Db 70 TDCADILLNGYRSGGYRIWPKSWMTVGTUNVYCDMETDGGTWTVIQRRNGTGNPSDYFY 129
 Qy 266 RTWODYKAGFNGRLRRFELGNDKIHLLTKSEMIILRIDLEDFNGVELYALYDQFYVANEF 325
 Db 130 KPMKNYKLGEGNTEKDFWLGNDRIFALTQNRNTMIRPDLKRENDTRYAIYQDFWJENED 189
 Qy 326 LKYRLHVGNYNGTAGDALRENKHYNHLKFFTTDPKDNDYPSGNCGLIYSSGWWFADCL 385
 Db 190 YLYCLHIGNYSGDAGNS--PGRINGHN---FSTIDKDHDTHT-HCAQTYKGGWYDRCH 243
 Qy 386 SANLNGKYYHQKRYGVVRNGLFTWGTGCVSEAHPGGYKSSFKKAMIRPKHF 437
 Db 244 ESNLNGIYLNGENSHYADGTEWRAWK-----GYHSLPQVEMKIRPVEF 287

[illegible]

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RESULT 14
Q9R045 ID Q9R045 PRELIMINARY; PRT; 493 AA.
AC Q9R045;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-RELATED PROTEIN-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9403103; PubMed=10473614;
RA Kim I., Moon S.O., Koh K.N., Kim H., Uhm C.S., Kwak H.J., Kim N.G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiotensin-
RT related protein, angiotensin-related protein induces endothelial cell
RT sprouting.";
RL J. Biol. Chem. 274:26523-26528(1999).
DR EMBL; AF125176; AAD55358.1; -.
DR HSP; P02671; IFLD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 493 AA; 57118 MW; 22885ABEF0746BF2 CRC64;

Query Match 20.4%; Score 485.5; DB 11; Length 493;
Best Local Similarity 30.8%; Pred. No. 1.6e-24;
Matches 117; Conservative 62; Mismatches 128; Indels 73; Gaps 12;

QY 66 IQLPKQSRIEVPEVKEV-----QNLKEIVNSLKKSCQDCQKLAQDNGDPGRNGLLIPSTGA 121
DB 170 LQLASKYKDLSEHKQHLAHLAHQNSQSEVIAQLSEHCQV-----PAARPMPQPPAA 220
QY 122 PGEVGD-----NRVLESEVANKLSSELNAKEEINVLHGRLEKLNLMNNTENYVDSKV 177
DB 221 PPRVYQPTTYNRI-----INQISNETQSQNLKVLPPSLPTPAL----- 261
QY 178 ANLFTFVNSLDGKSCPSQEQIQSRVQHLIYKDCSDYIAIGKRSSSETRYVTPDPKNSS 237
DB 262 -----TSLPSSDTKPSG-----WRDCLQALDGHSTSSYLYKVPENTNRL 302
QY 238 FEVYCDMETGGGWTVLQARLDGSTNFTWQDYKAGFGNLRREFWLGNDKIHLLTKSKE 297
DB 303 MOVWCDQRHDPGGWTVIQRLDGSVNFPRNWTYKQGFNGIDGFWLGLNIYWLNTQGN 362
QY 298 MILRLDLEDFNGVELYALYDQFYVANEFLKYLRLHVGNYNGTAGDALRFNKHYNHLKFFT 357
DB 363 YKLLVTMEDWGRKVFAYETASFLRPESEYKLRUGRYHGNAGDSFTW-----HNGKQPT 417
QY 358 TPDKDNDRYPGNCGLYYSSGWWFDCALSNLNGKYY---HOKYRGVRNGIFEWGTPGVS 414
DB 418 TLDLRDHDVY-TGNCAHYKGGKWWYNACAHSLNGLWYRGGHYRSR-YQDGVYWAEEFG--- 473
QY 415 EAHFGGKSSPKFAKMMIRP 434
DB 474 ----GSY--SLKKVVMIRP 487

RESULT 15
O08538 ID O08538 PRELIMINARY; PRT; 498 AA.
AC O08538;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE ANGIOPOIETIN-1 (ANG-1).

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GN ANGPT1 OR AGPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisompierre P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning.";
RL Cell 87:1161-1169(1996).
CC -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL; U83509; AAB50558.1; -.
DR HSP; P02671; IFLD.
DR MGD; MGI:108448; Agpt.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil.
FT DOMAIN 81 261 COILED COIL (POTENTIAL).
FT DOMAIN 284 498 FIBRINOGEN BETA/GAMMA.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC260D800 CRC64;

Query Match 20.3%; Score 483.5; DB 11; Length 498;
Best Local Similarity 31.7%; Pred. No. 2.2e-24;
Matches 127; Conservative 62; Mismatches 141; Indels 71; Gaps 14;

QY 61 LPPLTIQLPKQFSRIE-----EVFKVQNLKEIVNSLKKSCQDCQKLAQDNGDPGRN 112
DB 145 LTDVETQVLNQTSLRLEIQLENSLSTYKLEKQLLQQTNEILKTHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVANKLSSELNAKEEINVLHGR-----LEKMLNV 165
DB 192 SL-----EHLKEMEGKHKEELTLKEENLQGLVSRQTFIIQLEK-QLSR 239
QY 166 MNNIENVDSKVANLTFVNSLDGKCSK----CPSQEQIOSRPVQHLIYKDCSDYIAIGK 221
DB 240 ATNNNSILOKQQLLEMDTVHNLVSLCTKEGVLLKGGKREEKP-----FRCDADVQAGF 294
QY 222 RSSETYRV-----TPDPKNSSFVYCYDMETMGGWTVLQARLDGSTNFTWQDYKAGFGN 277
DB 295 NKSGLIYTFNNMPEPK-----KVFCDNVNGGWTVIQLHREDGSLDFQKWKYKMGFGN 350
QY 278 LRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYLRLHVGNYNG 337
DB 351 PSGEYWLGNFEIFAITSQRYQYMLRIELMDWEGNRAVSQYDRFRHIGNEKQNYRLYKLGHTG 410
QY 338 TAGDALRFNKHYNHLKFFFTTPDKDNDRYPGNCGLYYSSGWWFDCALSNLNGKYYHQ- 396
DB 411 TAGKQSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWVDFDAGCPNSLNGMFYTAG 465

```

QY 397 KYRGVRNGIFWGTWPGVSEAHPCGGYKSSFKKAKMMIRPKHF 437
: | | | | : | | : | | | |
Db 466 QNHGKLGINKWHYFKGPS-----YSLRSTTMMIRPLDF 498

Search completed: February 27, 2001, 12:49:35
Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:35 ; Search time 30.15 Seconds
(without alignments)
497.880 Million cell updates/sec

Title: US-09-442-143-2
Perfect score: 2378
Sequence: 1 MLANWYWLSSAVLATYGFLL.....GKSSFEKAKMIRPKHEKP 439
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:.*
1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT.*
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18: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	100.0	439	20	Human prothrombina
2	1853.5	77.9	432	20	Mouse prothrombina
3	524	22.0	314	15	Rat hepatic parench
4	522	22.0	496	17	Human TIE-2 ligand
5	522	22.0	496	17	Human TIE-2 ligand
6	522	22.0	496	19	Human TIE-2 ligand
7	522	22.0	496	21	Human angiotensin
8	522	22.0	496	21	Human angiotensin
9	521.5	21.9	498	19	Amino acid sequenc
10	517.5	21.8	499	19	Amino acid sequenc
11	506	21.3	312	17	Hepatocyte prolife
12	505.5	21.3	312	17	Hepatocyte prolife

13	505	21.2	491	20	Human zapo3 protei
14	505	21.2	491	20	Human TIE ligand N
15	505	21.2	491	21	Amino acid sequenc
16	505	21.2	491	21	An angiotensin-re
17	504.5	21.2	312	15	Human hepatic pare
18	500	21.0	491	21	Human secreted pro
19	489	20.6	346	20	Human AR-1 protein
20	489	20.6	346	20	Human TIE ligand N
21	487	20.5	496	19	Amino acid sequenc
22	487	20.5	497	17	Human TIE-2 ligand
23	487	20.5	497	17	Human TIE-2 ligand
24	487	20.5	497	19	Amino acid sequenc
25	486.5	20.5	498	17	Human TIE-2 ligand
26	486.5	20.5	498	17	Human TIE-2 ligand
27	486.5	20.5	498	19	Amino acid sequenc
28	486.5	20.5	498	21	Human angiotensin
29	486.5	20.5	498	21	Human angiotensin
30	483.5	20.3	494	19	Amino acid sequenc
31	481.5	20.2	453	16	Human fibrinogen g
32	481.5	20.2	453	16	Human fibrinogen g
33	480.5	20.2	493	20	Human TIE ligand N
34	480.5	20.2	493	21	PSEQ-3 protein enc
35	480.5	20.2	493	21	Human scarface 1 p
36	478.5	20.1	495	21	Angiotensin fusio
37	478.5	20.1	495	21	Angiotensin fusio
38	470.5	19.8	509	19	Mouse TIE-2 recept
39	469.5	19.7	509	19	Amino acid sequenc
40	468	19.7	411	16	Fibrinogen gamma c
41	461	19.4	491	16	Human fibrinogen B
42	460.5	19.4	461	21	Membrane-bound pro
43	460.5	19.4	509	20	TIE ligand-3 (TL3)
44	458.5	19.3	454	16	Partial human fibr
45	458	19.3	386	20	Human normal uteru

ALIGNMENTS

RESULT 1
W88235
ID W88235 standard; Protein; 439 AA.
XX
AC W88235;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human prothrombinase Fg12 protein.
XX
KW Prothrombinase; hfg12; human; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 179..183
FT Modified-site /label= Asn is N-glycosylated
FT Modified-site 235..238
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 262..265
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 336..337
FT Modified-site /note= "Asn is N-glycosylated"
FT Domain 213..439
FT Peptide /note= "fibrinogen related domain"
FT Peptide 364..378
FT Peptide /note= "epitope (Claim 4)"
XX
WO9851335-A1.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-CA00475.

```
XX PR 10-OCT-1997; 97US-0061684.
XX PR 15-MAY-1997; 97US-0046537.
XX PA (LEVY/) LEVY G.
XX PI Levy G;
XX XX
DR DR WPI; 1999-059687/05.
DR DR N-PSDB; V84139.
XX XX
XX XX Modulating immune coagulation - by using Fgl2 antibodies and
XX PT compounds, used to treat conditions including graft rejection and
XX PT foetal loss
XX XX
PS PS Claim 8; Page 66-67; 105pp; English.
XX XX
CC CC This is the amino acid sequence of human prothrombinase Fgl2, as
CC CC predicted from hfgl2 DNA (see V84139). Fgl2 is a 70 kDa
CC CC transmembrane serine protease that has immune procoagulant activity.
CC CC The invention provides a method for inhibiting immune coagulation by
CC CC inhibiting the activity or expression of Fgl2. The method can be
CC CC used in vivo to treat a condition which requires a reduction in
CC CC immune coagulation such as bacterial and viral infections, cancer,
CC CC glomerulonephritis, a number of gastrointestinal diseases,
CC CC allograft and xenograft rejection and foetal loss. An Fgl2-specific
CC CC antibody, an Fgl2 antisense oligonucleotide, or a substance that
CC CC affects prothrombinase activity of a Fgl2 protein may be used to
CC CC treat a condition requiring a reduction in procoagulant activity.
CC CC A vaccine containing an Fgl2 protein or peptide is used for
CC CC prevention of graft rejection or foetal loss (claimed).
XX XX
SQ Sequence 439 AA;

Query Match 100.0%; Score 2378; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 8.2e-206;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M KLANWYLSAVLATYGFLLVANNETEIKDERAKDVCVPRLSRGKCEEGECPYQVS 60
Db 1 m klanwywlsavlatygfllvanneteikderakdvcvpriesrgkceegecpyqvs 60

QY 61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLPSTG 120
Db 61 lppltiqlpkfrievevkevnleivnsllkscqcklqaddngdpgnglllpstg 120

QY 121 APGEVGDNRVRELESEVKNLSSELKNAKEEINVLHGRLEKLNLMNNTENYVDSKVANL 180
Db 121 apgevgdnrvrelesevnklselknakeeinvlhgrleklnlmnmnlenyvdskv anl 180

QY 181 TFVNSLDGKCSKPSQEQIOSRPVQHLYIKDCDYAYAGKSSERYRTPDPKNSSEFV 240
Db 181 tfvnsldgkcskpsqeqiolsrpvqhlyikcdsdyayagksseryrtpdpknssfev 240

QY 241 YCDMETMGGVTVLQARLDGSTNFTRTWODYKAGFCGNLRREFWLGNDKTHLLTKSEMIL 300
Db 241 ycdmetmggvtvlqarldgstnfttrtwodykagfgcnlrrrefwlgndkthlltksemil 300

QY 301 RIDLEDNGVELYALDYFYVANEFLKYRLHVGNYNGTAGDALRPNKHYNHDLLKFTTTPD 360
Db 301 ridledngvelyaldyfyvaneflkyrlhvgnyngtagdalrpnkhyndhllkftttd 360

QY 361 KDNDRYPGSGNGLYSSGWWFDCALISANLNGKYHOKYRGVNGIFWGTWPGVSEAHPGG 420
Db 361 knddrypsngncllyssgwwfdcalsanlngkyhokyrgvngifwgtwpgvseahpgg 420

QY 421 YKSSFKEAKMMIRPKHFKP 439
Db 421 ykssfkeakmmirpkhfkp 439
```

RESULT 2

```
W88236
ID W88236 standard; Protein; 432 AA.
XX AC W88236;
XX DT 15-MAR-1999 (first entry)
XX DE Mouse prothrombinase Fgl2 protein.
XX XX
KW Prothrombinase; Fgl2; mouse; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine.
XX OS Mus sp.
XX XX
FH Key Location/Qualifiers
FT Modified-site 172..174
FT /label= Asn is N-glycosylated
FT Modified-site 228..231
FT /note= "Asn is N-glycosylated"
FT Modified-site 256..259
FT /note= "Asn is N-glycosylated"
FT Modified-site 323..325
FT /note= "Asn is N-glycosylated"
FT Domain 213..439
FT /note= "fibrinogen related domain"
XX XX
XX W09851335-A1.
XX 19-NOV-1998.
XX PF 15-MAY-1998; 98WO-CA00475.
XX XX
XX 10-OCT-1997; 97US-0061684.
XX 15-MAY-1997; 97US-0046537.
XX PA (LEVY/) LEVY G.
XX XX
XX Levy G;
XX WPI; 1999-059687/05.
XX N-PSDB; V84140.
XX XX
XX Modulating immune coagulation - by using Fgl2 antibodies and
XX PT compounds, used to treat conditions including graft rejection and
XX PT foetal loss
XX XX
PS Claim 8; Page 70-71; 105pp; English.
XX XX
CC This is the amino acid sequence of mouse prothrombinase Fgl2, as
CC CC predicted from fgl2 DNA (see V84140). Fgl2 is a 70 kDa
CC CC transmembrane serine protease that has immune procoagulant activity.
CC CC The human Fgl2 amino acid sequence is given in W88236. The
CC CC invention provides a method for inhibiting immune coagulation by
CC CC inhibiting the activity or expression of Fgl2. The method can be
CC CC used in vivo to treat a condition which requires a reduction in
CC CC immune coagulation such as bacterial and viral infections, cancer,
CC CC glomerulonephritis, a number of gastrointestinal diseases,
CC CC allograft and xenograft rejection and foetal loss. An Fgl2-specific
CC CC antibody, an Fgl2 antisense oligonucleotide, or a substance that
CC CC affects prothrombinase activity of a Fgl2 protein may be used to
CC CC treat a condition requiring a reduction in procoagulant activity.
CC CC A vaccine containing an Fgl2 protein or peptide is used for
CC CC prevention of graft rejection or foetal loss (claimed).
XX XX
SQ Sequence 432 AA;
```

```
Query Match 77.9%; Score 1853.5; DB 20; Length 432;
Best Local Similarity 77.7%; Pred. No. 1.4e-158;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

QY 1 M KLANWYLSAVLATYGFLLVANNETEIKDERAKDVCVPRLSRGKCEEGECPYQVS 60
```

Db	1	mrlpgwllwsavlaacr-aveehnltegladasagaacparlegsrc-egsqcpqfqt	58
Qy	61	LPPtIQLPQFSRIEEVFKEVQNLEIVNSLKSQCDCQLAQQNDGDPGRNGLLIPTSG	120
Db	59	Iptitqlprqlsgmeevlkevrtlkeavdsllkscqcdklqadhdrgpgng---	gng 114
Qy	121	APGEVDNRVRLESEYVNKLSSSELKNAKEINVHGRLEKLNLVNMNTENTYDVSKANL	180
Db	115	ae-taedsrvqelesgvnklsselnakddlgqlgrletlhvlmnmnienvydnkanv	173
Qy	181	TfVVNSLDGCKSPSQEOIQSRPVQHLYVKDCSDYYAIGKRSETYRYVPDPKNSSFEV	240
Db	174	tvvnsldgckspcqhmgspvbhllykdcsdhvlygrtssgayrvtvdhrnssf	233
Qy	241	YCDMETGGGWTVLQARLDGSTNFTRTWODYKAGFGNLRREFWLGNDKTHLLTKSKEMIL	300
Db	234	ycdmetmggwttvlgarlvgstnftrwdkydagfgnlerefwlgndkthlltkskemil	293
Qy	301	RIDLEDENGVELYALYDOFYVANEFLKYRLHVGCNYNGTAGDALRENKHYNHDLKEFTTPD	360
Db	294	ridledengtlalydqfyvaneflkyrlhvngntagdalrfsrhynehdlrfttpd	353
Qy	361	KDNDRYPSCGCLYSSGWWFDACL SANLINGKYHYOKYGVRRNGIFWGTFWPGVSAHPGG	420
Db	354	rndrypsncglysssgwwfdclsanlingkyhyokygvrngifwgtwpjngaqpgg	413
Qy	421	YKSSFKEAKMIRPKFKP	439
Db	414	ykssfkqakmmirpkfnkfp	432

RESULT	3
R65759	R65759 standard; protein; 314 AA.
XX	
XX	R65759;
XX	
DT	17-MAY-1995 (first entry)
XX	
DE	Rat hepatic parenchymal cell growth factor.
XX	
KW	Hepatic parenchymal cell growth factor; HPGF; liver diseases;
KW	liver cancer; cirrhosis.
XX	
OS	Rattus rattus.
XX	
XX	
FH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..24
FT	/label= sig_peptide
XX	
XX	WO9421678-A.
PN	
XX	
XX	29-SEP-1994.
XX	
XX	22-MAR-1994; 94WO-JP00455.
PF	
XX	
XX	23-MAR-1993; 93JP-0063905.
PR	
XX	
XX	(TAIS) TAISHO PHARM CO LTD.
PA	
XX	
XX	Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;
PI	
XX	
XX	WPI; 1994-316940/39.
DR	N-PSDB; Q77818.
XX	
XX	
PT	Hepatic parenchymal cell growth promoter peptide - is isolated
PT	from human or animal liver cell or produced by recombinant
PT	techniques and used for therapy of liver diseases
XX	
XX	Claim 3; Page 34; 47pp; Japanese.
PS	
XX	
CC	Q77818 encodes R65759 rat hepatic parenchymal cell growth factor (HPGF)

CC The protein or the N-terminal peptide (R65758) may be used in the
CC diagnosis and treatment of liver diseases, such as liver cancer and
CC cirrhosis.

Query Match	22.08;	Score	524;	DB	15;	Length	314;
Best Local Similarity	37.68;	Pred.	No. 4.3e-39;				
Matches	124;	Conservative	46;	Mismatches	104;	Indels	56;
Gaps							
Qy	125	VGD--NRVRE---	LESEVKNLSSELKNAKEEI-NVLHGRLEKLNLMNNNIENYVDSKVAN	179			
Db	23	lgdenciqevrlraqvrlqetrvkqgvviagllhek--evflldrgqedsfid----	75				
Qy	180	LTFVYNSLDGCKSCPCSQEQIQSRVPVQHLHYKDCSDYIAIGKRSSSTYRTPDPKNSPSE	239				
Db	76	-----lggk-----	rh--yadcseilyndgfkhsyfykikplqslaeafs	111			
Qy	240	VYCDMETWGGGWTVLQARLDGTSNFTTWODYRAGFNL---	RREFWLGNDKIHLHTKSK	296			
Db	112	vyccmsd--gggwtvltqrsdgsenfngwdyngfngvsgngeywlgnkninlltmgd	170				
Qy	297	EMILRIDLEDFNGVELYALYDOFVVAEEFLKYRLHGVNGTGTAGDALRENKH----	YN	350			
Db	171	dytklidltdfeknsrfaqyekfkvgdeksefyelngeysgtagslsgtfhpveqawas	230				
Qy	351	HDLKFFFTPPDKNDRPSGNGCLYYSGGWFDACL SANLNGKYHYHOKYRG--VRNGFTWGT	409				
Db	231	hqtmkfstdrdnony-ngnceaeegsgwwfnrchsanlngyyyqpyraetdngvvywt	289				
Qy	410	WPGVSEAHPGGYKSSFKFEAKMMTRPKHFKP	439				
Db	290	w-----tqwwslksvnmklrpsdfip	311				

RESULT	4	
W01411		
ID	W01411	standard; Protein; 496 AA.
XX	XX	
XX	AC	
XX	W01411;	
XX	XX	
DT	11-FEB-1997	(first entry)
XX	XX	
DE	Human TIE-2	ligand 2.
XX	XX	
XX	TIE-2	ligand 2; tyrosine kinase with Ig and EGF homology domain; receptor; antagonist; neovascularisation; wound healing; ischaemia; leukopaenia; thrombocytopenia; anaemia; angiogenesis; tumour atherosclerosis; inflammation; diagnosis; therapy.
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	W09631	1598-A1.
XX	XX	
PD	10-OCT-1996.	
XX	XX	
PF	05-APR-1996;	96WO-US04806.
XX	XX	
PR	06-OCT-1995;	95WO-US12935.
PR	06-APR-1995;	95US-0418595.
XX	XX	
PA	(REGE-) REGENERON PHARM INC.	
XX	XX	
PI	Aldrich TH, Bruno J, Davis S, Goldfarb M, Jones PF;	
PI	Maisonpierre PC, Radziejewski C, Yancopoulos GD;	
XX	XX	
DR	WPI: 1996-465021/46.	
DR	N-PSDB: T44321.	
XX	XX	
PT	TIE-2	agonists and antagonists and related DNA - useful for promoting or blocking neovascularisation, etc

[illegible]

```

Db 375 lkdwegneasyehfylsseelnryrhlkglgtagkissisqpgnd----fstkdgdn 430
QY 364 DRYPSGNCGLYSSGWFDAACLSANLKGYYHOKYRGVR-NGIFWGTWPGVSEAHPPGYK 422
Db 431 dkci-cscqmlggwfdacgpnlnmgypqrqntknfngikwywkg-----sgy- 482
QY 423 SSFKEAKMIRPKHF 437
Db 483 -slkattmmirpadf 496

RESULT 6
W47532
ID W47532 standard; Protein; 496 AA.
XX
AC W47532;
XX
DT 09-SEP-1998 (first entry)
XX
DE Human TIE-2 ligand 2 from clone pBluescript KS.
XX
KW Chimeric TIE ligand 2NICIF; TIE-2 ligand; neovascularisation;
KW tumour; human.
XX
OS Homo sapiens.
XX
PN WO9805779-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13557.
XX
PR 25-OCT-1996; 96US-0740223.
XX
PR 02-AUG-1996; 96US-0022999.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
WPI; 1998-145615/13.
DR N-PSDB; V18619.
XX
Modified human TIE-2 receptor ligand(s) - useful for promoting wound
healing
XX
Example 8; Fig 6; 202pp; English.
XX
This is the amino acid sequence of the human TIE-2 ligand 2,
used in the method of the invention, involving the production
of TIE-2 ligands which promote healing. The nucleic acids, vectors
and host cells used in the method of the invention are useful for
the recombinant production of the ligands. The ligands, etc. are
useful for blocking blood vessel growth, promoting neovascularisation,
promoting the growth or differentiation of a cell expressing the TIE
receptor, blocking the growth or differentiation of a cell expressing
the TIE receptor and for attenuating or preventing tumour growth in
a human.
XX
Sequence 496 AA;

```

Query Match 22.0%; Score 522; DB 19; Length 496;
 Best Local Similarity 27.9%; Pred. No. 1.3e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

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QY 43 LFSRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 mdsidkkyqvgngscsytlflpemdnrcrsssspyvsnvdrpadleyddsvqlrglen 85
QY 85 LKE-----IVNSLKKSCQDCKLQADNDGDPGRNGLLPLSPGAPGEVDN---- 128
Db 86 lnenntqwlmklenyiqdmkkmveiqqnavqn-----qtavmiegtlnlq 134

```

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QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
Db 135 taeqrkltdveaqvlnqtrielqllehslnstnkleqildqtseinklqdknsflekk 194
QY 162 NLV-----NNNTIENVDSKVANLTF-----V 183
Db 195 vlamedkhiqlgsikeekdqivsvskqnsileekkiivatvnnsvlqkqhdmet 254
QY 184 VNSLDGKCKSPSQIQSRPVQHLLYKDCSDYYAIGKRSEYRYVTPDPKNSSEVYCD 243
Db 255 vnnlittmstnsakdprvakeeqisfrdcaeavfksghtngiytltfpnsteelxaycd 314
QY 244 METMGGWTVLQARLDGSTNFTRTWQYKAGFGNLRERFEWLGNDKIHLLTKSEMILRID 303
Db 315 meaggvgwtiqrredgsdvtqrwkekykvfgnpsgeywlgnfvsqldnqgryvlkih 374
QY 304 LEDFNGVELYALYDOFYVANEFELKYRLHVGNYNGTAGDALRKNKYNHDLKFFTPDKDN 363
Db 375 lkdwegneasyehfylsseelnryrhlkglgtagkissisqpgnd----fstkdgdn 430
QY 364 DRYPSGNCGLYSSGWFDAACLSANLKGYYHOKYRGVR-NGIFWGTWPGVSEAHPPGYK 422
Db 431 dkci-cscqmlggwfdacgpnlnmgypqrqntknfngikwywkg-----sgy- 482
QY 423 SSFKEAKMIRPKHF 437
Db 483 -slkattmmirpadf 496

RESULT 7
Y78903
ID Y78903 standard; Protein; 496 AA.
XX
AC Y78903;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human angiotensin-2 amino acid sequence.
XX
KW Angiotensin-2; Ang-2; vascular endothelial growth factor; tumour;
KW vascularisation; angiogenesis; blood vessel maturation; malignant;
KW benign; binding ligand; cancer; aminophospholipid.
XX
OS Homo sapiens.
XX
PN WO200002587-A1.
XX
PD 20-JAN-2000.
XX
PF 12-JUL-1999; 99WO-US15668.
XX
PR 13-JUL-1998; 98US-0092589.
XX
PR 02-DEC-1998; 98US-0110600.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Thorpe PE, Ran S;
XX
WPI; 2000-182177/16.
DR N-PSDB; 292213.
XX
Binding ligand for aminophospholipid used in the treatment of
vascularised tumours, comprises targeting component and therapeutic
agent -
XX
Disclosure; Page 257-259; 267pp; English.
XX
This sequence represents the human angiotensin-2 (Ang-2) amino acid
sequence. Ang-2 is a naturally occurring angiogenesis antagonist when
vascular endothelial growth factor (VEGF) levels are low, and generally
counteracts the blood vessel maturation and stability mediated by Ang-1.
Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation
or stabilisation factor, converting immature vessels to mature vessels.
CC

```


Db 431 dkci-c-kcsqmltgwfdacgpnlnmgypqqrntkfnkgikwywkg-----sgy- 482

QY 423 SSFKEAKMMIRPKHF 437

Db 483 -slkattmmirpadf 496

RESULT 9

W47528

ID W47528 standard; Protein; 498 AA.

XX

AC W47528;

XX

DT 09-SEP-1998 (first entry)

XX

DE Amino acid sequence of chimeric TIE ligand INIC2F (chimera 1).

XX

KW Chimeric TIE ligand INIC2F; TIE-2 ligand; neovascularisation;

KW tumour; human.

XX

OS Homo sapiens.

XX

PN W09805779-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-US13557.

XX

PR 25-OCT-1996; 96US-0740223.

PR 02-AUG-1996; 96US-0022999.

XX

PA (REGE-) REGENERON PHARM INC.

XX

PI Davis S, Yancopoulos GD;

XX

DR WPI; 1998-145615/13.

DR N-PSDB; V18615.

XX

PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound healing

PT

PS Claim 20; Fig 24; 202pp; English.

XX

CC This is the amino acid sequence of the chimeric TIE ligand INIC2F,

CC used in the method of the invention, involving the production

CC of TIE-2 ligands which promote healing. The nucleic acids, vectors

CC and host cells used in the method of the invention are useful for

CC the recombinant production of the ligands. The ligands, etc. are

CC useful for blocking blood vessel growth, promoting neovascularisation,

CC promoting the growth or differentiation of a cell expressing the TIE

CC receptor, blocking the growth or differentiation of a cell expressing

CC the TIE receptor and for attenuating or preventing tumour growth in

CC a human.

XX

SQ Sequence 498 AA;

Query Match 21.9%; Score 521.5; DB 19; Length 498;

Best Local Similarity 32.7%; Pred. No. 1.5e-38;

Matches 131; Conservative 61; Mismatches 138; Indels 71; Gaps 14;

QY 61 LPLTLTLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDKLQADDNGDPGRN 112

Db 145 ldtvetqlnqtrleiglenslstkykleqlqgtnelike-----kn 191

QY 113 GLLLPSTGAPCEVDNRVRESEVNKLSELKNAKEINVLHG-----RLEK-L 161

Db 192 slt-----ehkilene---ghkkeltdlkekenlglvtrqtyiigeleql 237

QY 162 NLVNMMNIENVDSKAVNLTFVNSLKGKSK-----CPSQBIQSRPVOHLIYKDCSDYY 217

Db 238 nrattnn--svlqkqqlmdvtvnlvnlctkegvlkkgkreep-----frdcaevf 290

QY 218 AICKRSSTRYVTPDPKNSSEFVYCDMETMGGWTVLQARLDGSTNFTRTWQDYKAGFGN 277

Db 291 ksghtngiytlftfnsteeikaycdmeaggggtliqirredgsdvdftrtwkeykvvgfn 350

QY 278 LRREFWLGNDKIHLLTKSKEMILRIDLEDPNGVELYALYDOFYVANEFLKYRLHVGNYNG 337

Db 351 psgeywlgnfvsqnltnqgrvylkhlkdwegneayslyedfylsseeinryrlhkgltg 410

QY 338 TAGDALRFNKHYNHDLKFFTTDPKDNDRYPSGNCGLYYSGWMFDCLSANLNGKYVHOK 397

Db 411 tagkissisqgnd----fstkdgdndkcic-kcsgmltgwfdacgpnlnmgypqr 465

QY 398 YRGVR-NGIFWGTWPGVSEAHPGGYKSSPKFAKMMIRPKHF 437

Db 466 qntnkfngikwywkg-----sgy--slkattmmirpadf 498

RESULT 10

W47529

ID W47529 standard; Protein; 499 AA.

XX

AC W47529;

XX

DT 09-SEP-1998 (first entry)

XX

DE Amino acid sequence of chimeric TIE ligand IN2C2F (chimera 3).

XX

KW Chimeric TIE ligand IN2C2F; TIE-2 ligand; neovascularisation;

KW tumour; human.

XX

OS Homo sapiens.

XX

PN W09805779-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-US13557.

XX

PR 25-OCT-1996; 96US-0740223.

PR 02-AUG-1996; 96US-0022999.

XX

PA (REGE-) REGENERON PHARM INC.

XX

PI Davis S, Yancopoulos GD;

XX

DR WPI; 1998-145615/13.

DR N-PSDB; V18616.

XX

PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound healing

PT

PS Claim 20; Fig 26; 202pp; English.

XX

CC This is the amino acid sequence of the chimeric TIE ligand IN2C2F,

CC used in the method of the invention, involving the production

CC of TIE-2 ligands which promote healing. The nucleic acids, vectors

CC and host cells used in the method of the invention are useful for

CC the recombinant production of the ligands. The ligands, etc. are

CC useful for blocking blood vessel growth, promoting neovascularisation,

CC promoting the growth or differentiation of a cell expressing the TIE

CC receptor, blocking the growth or differentiation of a cell expressing

CC the TIE receptor and for attenuating or preventing tumour growth in

CC a human.

XX

SQ Sequence 499 AA;

Query Match 21.8%; Score 517.5; DB 19; Length 499;

Best Local Similarity 28.1%; Pred. No. 3.4e-38;

Matches 133; Conservative 73; Mismatches 166; Indels 101; Gaps 13;

QY 44 ESRGKCEAGECPYQVSL-----PLTLTLPKQFSRIEVEFKEVQNLKEIVNSLKK 94

Db 49 ehgncresttdqyntnalqrdaphvdpdsvqrlqvlennime--nntqwlmklenyiqd 106
 Qy 95 SQDCCKLQADDNGDPGRNGLLPSTGAPGEVGDN-----RVRELESEV----- 137
 Db 107 nmkkemveiqgnvqngtavmi-----eigtlnlntqtaeqtrkitdveaqvlnqtrtl 159
 Qy 138 -----NKLSELNAKEEINVHGR---LEKLNIV----- 164
 Db 160 elqllehlstnklekqildtseinklqdknsflekvlamedkhiilqlsqikeekdql 219
 Qy 165 -----NMNINIYVDSKANLTF-----VNSLDGCKGCKPQBOIQSRPV 205
 Db 220 qvlsvkqnsiieelekkivtatvnnsvlqkqhdmetvnnlltmmstnsakdptvake 279
 Qy 206 QHLIYKDCSDYYAIGKRSEYRTVPDPKNSSEFYVCDMETGGGWTVLQARLDGSTNFT 265
 Db 280 eqisfrdcaevfksgtngtiyltfnsteeikaycdmeagggwtliqrredgsvdfq 339
 Qy 266 RTWDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDOFYVANEF 325
 Db 340 rtwkeykvfgnpsgeywiqnefvsgltnqqrlyvklhikdwegneayslyehfyssee 399
 Qy 326 LKYLHVGNNGYNTAGDALRFNKHYNHDLKFFTPDKDNDRYPSGNCGLYYSSGWWFDACL 365
 Db 400 lnyrhlkgltgtagkissisqpgnd-----fscdgdndkcic-kcsqmltggwvfdacg 434
 Qy 386 SANLNGKYYHOKYRGVVR-NGIFWGTWPGVSEAHPPGGYKSFKEAKMIRPKHF 437
 Db 455 panlmgmyypqrntnknfngikwywkg-----sgy--slkattmmirpadf 499

RESULT 11

R94317
 ID R94317 standard; Protein; 312 AA.

XX AC R94317;

XX DT 05-NOV-1996 (first entry)

XX DE Hepatocyte proliferation substance HP-041V.

XX KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;

XX KW chinese hamster ovary cell; CHO; hepatitis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide

XX FT /note= "signal peptide"

XX FT 23..312

XX FT Protein

XX FT /note= "mature protein"

XX PN WO9609383-A1.

XX XX 28-MAR-1996.

XX XX 21-SEP-1995; 95WO-JP01904.

XX XX 22-SEP-1994; 94JP-0228234.

XX XX (TAIS) TAISHO PHARM CO LTD.

XX XX Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;

XX XX WPI; 1996-188445/19.

XX DR N-PSDB; T13397.

XX XX

PT Vector for expression of hepatocyte proliferation substance - in
 PT eukaryotic cells, used as diagnostic reagent for hepatitis and for
 PT basic research on in vitro liver cell cultures

XX PS Example 3; Page 28-29; 44pp; Japanese.

XX XX

CC This is the amino acid sequence of a variant human hepatocyte
 CC proliferation substance (HPS). The variant differs from the sequence
 CC encoded by T13396 at pos. 214: A to G change and pos. 314: T to C. These
 CC changes alter the amino acid residues at pos. 50 of the mature protein:
 CC Ile to Val and pos. 83: Leu to Pro. The gene was isolated from a
 CC lambda-gt10 human cDNA library using the sequence T13396 as a probe.
 CC The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which
 CC was subsequently recombined to produce plasmid pCDLH-dhir in which the
 CC HPS gene is under control of the SR-alpha promoter. This plasmid is
 CC transformed into CHO cells to express the HPS protein. The HPS protein
 CC can be used to diagnose hepatitis.

XX Sequence 312 AA;

Query Match 21.3%; Score 506; DB 17; Length 312;

Best Local Similarity 44.6%; Pred. No. 1.8e-37;

Matches 107; Conservative 25; Mismatches 88; Indels 20; Gaps 6;

Qy 210 YKDCSDYYAIGKRSEYRTVPDPKNSSEFYVCDMETGGGWTVLQARLDGSTNFTWQ 269
 Db 80 yadceifndgyklsqykikplqspaeefsvcdmsd-gggwtvqrrsdgsenfngwk 138

Qy 270 DYKAGFNL---RREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDOFYVANEFL 326
 Db 139 dyengfgnfvqkhegywlgknlnhflttqedytlkidladfeknsryaqyknfvkgdekn 198

Qy 327 KYRLHVGNNGYNTAGDALRFNKH-----YNHDLKFFTPDKDNDRYPSGNCGLYYSSGWW 380
 Db 199 fyelnigeysgtagdsagnfhpevwashqrmkfstwdrhdny-egnceaedqsgww 257

Qy 381 FDACLSANLNGKYYHOKYRGVVR-NGIFWGTWPGVSEAHPPGGYKSFKEAKMIRPKHF 439
 Db 258 fnrchsanlmgvyypqytaktngivwtw-----hgwwylksvnmktrpndfip 309

RESULT 12

R94316
 ID R94316 standard; Protein; 312 AA.

XX AC R94316;

XX DT 05-NOV-1996 (first entry)

XX DE Hepatocyte proliferation substance HP-041.

XX KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;

XX KW chinese hamster ovary cell; CHO; hepatitis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide

XX FT /note= "signal peptide"

XX FT 23..312

XX FT Protein

XX FT /note= "mature protein"

XX PN WO9609383-A1.

XX XX 28-MAR-1996.

XX XX 21-SEP-1995; 95WO-JP01904.

XX XX 22-SEP-1994; 94JP-0228234.

XX XX (TAIS) TAISHO PHARM CO LTD.

XX XX Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;

XX XX WPI; 1996-188445/19.

XX DR N-PSDB; T13396.

XX XX

PT Vector for expression of hepatocyte proliferation substance - in

FT eukaryotic cells, used as diagnostic reagent for hepatitis and for
 PT basic research on in vitro liver cell cultures

XX Claim 2; Page 23-24; 44pp; Japanese.

XX This is the amino acid sequence of a human hepatocyte proliferation
 CC substance (HPS). The gene encoding the HPS was isolated from a
 CC lambda-gt10 human cDNA library using a fragment of the corresp. rat gene
 CC as a probe (sequence not given in the specification). The human gene was
 CC cloned in plasmid pSCL to produce plasmid pSVLH which was subsequently
 CC recombined to produce plasmid pCDLH-dhr in which the HPS gene is under
 CC control of the SR-alpha promoter. This plasmid is transformed into CHO
 CC cells to express the HPS protein. The HPS protein can be used to diagnose
 CC hepatitis.

XX Sequence 312 AA;

Query Match 21.3%; Score 505.5; DB 17; Length 312;
 Best Local Similarity 36.8%; Pred. No. 2e-37;
 Matches 119; Conservative 40; Mismatches 119; Indels 45; Gaps 10;

QY 131 RELESEVKNLSSELNKAKEINVLHGRLE-----KLNLMNMNIENYVSKYANLTFVYVNS 186

Db 18 rei-saledcaqcmrlraqvrlletrvkqgkvkikqlqllqenevqfkdkgdentvidlg- 75

QY 187 LDGCKSCPQEQIQSRVQHLIYKDCSDYYAIGKRSETYRVTPDPKNSSEFYVCDMET 246

Db 76 -----skrq-----yadceifndgkysgfykikplqlqlaefsvycdmsd 116

QY 247 MGGWTVLQARLDGSTNFTRWODYKAGFGLN---RREFWLGNDKIHLTKSKEMILRID 303

Db 117 -ggwtvqrrdsqsnfnrgwkdyngfnvqkghyewlgnknlhlttqedytlkld 175

QY 304 LEDFNGVELYALYDQFYVANEFLKYLRLHVGNYNGTAGDALRPNKH-----YNHDLKFFT 357

Db 176 ladfeknsryaqkknfvgdekfnfelnigysgtagslagnfhpeqvqwasqrmkfs 235

QY 358 TPKDNDRIYPSGNGCLYYSGWFDACLSANLNGKYTHQKTRG-VRNGIFWGTWPGVSEA 416

Db 236 twdrhdny-egncaeedqsgwfnrchanlmgvyysgpytaktngivvtyw----- 288

QY 417 HPGGYKSSPFEAKMMIRPKFKP 439

Db 289 --hgwwylksvnmkrrpnafip 309

RESULT 13

Y26196

ID Y26196 standard; Protein; 491 AA.

XX AC

XX Y26196;

DT 03-NOV-1999 (first entry)

XX DE Human zapo3 protein.

XX KW Human zapo3 protein; angiotensin-1; angiotensin-2; covalently linked;

KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;

KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiogenic;

KW haematopoietic; mitogenic activity; angiogenesis; inhibitor;

KW endocrine-vascular cell association; revascularisation; DNA probe;

KW neuronal degeneration; anti-zapo3 antibody.

XX OS Homo sapiens.

XX FH Location/Qualifiers

XX Key 1..21

XX Peptide /label= Secretory_Signal_Sequence

XX Peptide 43..48

XX Peptide /label= Immunogen

XX Peptide /note= "For production of antibodies"

XX Peptide 93..98

FT /label= Immunogen

FT /note= "For production of antibodies"

FT 120..125

FT /label= Immunogen

FT /note= "For production of antibodies"

FT 421..426

FT /label= Immunogen

FT /note= "For production of antibodies"

FT 422..427

FT /label= Immunogen

FT /note= "For production of antibodies"

FT 279..490

FT /label= Fibrinogen-like domain

FT /note= "Homologous to residues 631-864 of human

FT fibrinogen alpha chain "

FT 63..253

FT /label= Amino-terminal_coiled_coil_domain

FT Misc-difference 280

FT /note= "Conserved cysteine residue"

FT Misc-difference 309

FT /note= "Conserved cysteine residue"

FT Misc-difference 432

FT /note= "Conserved cysteine residue"

FT Misc-difference 445

FT /note= "Conserved cysteine residue"

XX WO9940193-A1.

XX 12-AUG-1999.

XX 03-FEB-1999; 95WO-US02303.

XX 04-FEB-1998; 98US-0018258.

XX (ZYMO) ZYMOGENETICS INC.

XX Holloway JL, Shoemaker KE;

XX WPI; 1999-508503/42.

XX N-PSDB; X80866.

XX Human angiotensin homologue, ZAPO3 useful for study and regulation

XX of angiogenesis

XX Claim 1; Page 65-67; 78pp; English.

XX The present sequence is a human zapo3 protein. Zapo3 protein exhibits

XX significant amino acid sequence homology to angiotensin-1 and 2. It is

XX covalently linked to a moiety chosen from affinity tags, toxins,

XX radionuclides, enzymes and fluorophores. The protein is assembled as a

XX multimer and is characterized by an amino-terminal coiled coil domain and

XX a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,

XX haematopoietic and mitogenic activity. It is useful in the study and

XX regulation of angiogenesis, and for developing inhibitors of

XX angiogenesis. It is possibly involved in modulation of endocrine-vascular

XX cell association and may be used therapeutically to stimulate the

XX revascularisation of tissue, to promote angiogenesis and prevent neuronal

XX degeneration. DNA probes and anti-zapo3 antibodies can be used to detect

XX sites of angiogenesis.

XX Sequence 491 AA;

XX Query_Match 21.2%; Score 505; DB 20; Length 491;

XX Best Local Similarity 26.9%; Pred. No. 4.4e-37;

XX Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

QY 47 GKCEAGECPYQVSLPPLTIQLP-----KQFSRIEEVF--KEYQNLKEIVNSLKSKQ 97

Db 42 gk-eaakcaytflvpegritgpcvntkqgdstkdmtdienlkdvlsrqkred 100

QY 98 DCKLOADNDGPGNRGNLLLPSTGAPGEVGDNRVRELESEVKNLSSELKNAKEINVLHGR 157

Db 101 vlqlvvdvgn-----ivnevkllrkesnmnsrvtqlmq 136
 Qy 158 L-----EKLNLVNMNNIENV-----DSKVANLTFVYVNS-----L 187
 Db 137 llheirkrdslelsqlenkilnvttemlkmatriylevkvysitdivnqgsvmitll 196
 Qy 188 DGKCKSPQEQIQSRP-----VQHL----- 208
 Db 197 eeqlrfrsqdthvspplvqvpphpnsgqytpgllgngneiqrdpgyprdlmppedla 256
 Qy 209 -----IYKDCSDYYAIGKRSSSTYRVTDPKPKNSFEVYCDMETMGG 249
 Db 257 tsptkspfkippvtfinepfkdcqakeaghsvsgiymlkpenngpmqlwcnslldpg 316
 Qy 250 GWTVLQARLDGSTNFTRTWQDYKAGFNLRRFNLGNDKIHLLTKSKEMILRLIDLEDFNG 309
 Db 317 gwtvlgkrtgdgsvnfrrwnyknkgfngidgwyglglenymisnqndnykllieledwsd 376
 Qy 310 VELYALYDOFYVANEFLKYLRLHVGNYNGTAGDALRPNKHYNHDLKFFTPDKNDNDYPSG 369
 Db 377 kkvyaeysfrlepeseefyrlrlgtvggnagdsmmw-----hngkqftldrdkdm-ag 430
 Qy 370 NCGLYSSGWFFDACLSANLNGKIYH-QKRGV-RNGIFWGTWPGVSEAHPGYKSSFEKE 427
 Db 431 ncahfkggwynacahsnlmgvyrghyrskhgqdgifwaeyrg-----gsy--slra 482
 Qy 428 AKMMIRP 434
 Db 483 vqmmikp 489

RESULT 14

Y05397
 ID Y05397 standard; Protein; 491 AA.

XX Y05397;

AC Y05397;

XX Y05397;

DT 01-JUL-1999 (first entry)

DE Human TIE ligand NL5 protein sequence.

XX Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis;

KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
 KW early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
 KW endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
 KW vasculogenesis; detection; diagnosis; therapy.

XX Homo sapiens.

OS W09915653-A2.

PN 01-APR-1999.

PD 14-SEP-1998; 98WO-US19093.

XX 29-OCT-1997; 97US-0960507.

PR 19-SEP-1997; 97US-0933821.

XX (GETH) GENENTECH INC.

PA Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;

XX Hillan K, Roy M, Schwall R, Tumas D;

XX WPI; 1999-263480/22.

DR N-PSDB; X36342.

XX New isolated TIE ligand homologs for, e.g. developing products for

PT treatment of tumors

XX Claim 8; Fig 5; 132pp; English.

PS This sequence is the human tyrosine kinase containing Ig and EGF

XX homology domains (TIE) ligand of the invention, designated NL5.

CC Human; angiopoietin; HANG; Incyte Clone 2365223; cardiovascular disorder;

CC The TIE receptors are receptor tyrosine kinases which are expressed in
 CC vascular endothelial cells and early haemopoietic cells. The TIE
 CC receptors are believed to be actively involved in angiogenesis, and may
 CC play a role in haemopoiesis as well. The TIE ligand homologs can promote
 CC the survival and/or growth and/or differentiation of TIE receptor
 CC expressing cells. They can be used for promoting neovascularisation in
 CC wound healing and for promoting angiogenic processes, such as for
 CC inducing collateral vascularisation in an ischaemic heart or limb, or for
 CC promoting bone development and/or maturation and/or growth in a patient
 CC or muscle growth and development. The TIE ligand homologs and antibodies
 CC can inhibit the growth of endothelial cells and induce apoptosis of
 CC cells, particularly tumour cells. They can inhibit vasculogenesis,
 CC particularly the vascularisation of tumour cells. The antibodies can also
 CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,
 CC NL8 or NL4 polypeptide is amplified. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic
 CC animals.

XX Sequence 491 AA;

Qy Query Match 21.2%; Score 505; DB 20; Length 491;

Best Local Similarity 26.9%; Pred. No. 4.4e-37;

Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

Qy 47 GKCEEAGECPYQVSLPPLTTQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97

Db 42 gk-eeakkcaytfivpegritgpcvntkqgdastikdmtrmdlenlkdvlsrqkreid 100

Qy 98 DCKLOADDNGDPGRNLLLPSTGAPGEVGDNRVRELSEVKNLSSELKNAKEEINVLHGR 157

Db 101 vlqivvdvgn-----ivnevkllrkesnmnsrvtqlmq 136

Qy 158 L-----EKLNLVNMNNIENVV-----DSKVANLTFVYVNS-----L 187

Db 137 llheirkrdslelsqlenkilnvttemlkmatriylevkvysitdivnqgsvmitll 196

Qy 188 DGKCKSPQEQIQSRP-----VQHL----- 208

Db 197 eeqlrfrsqdthvspplvqvpphpnsgqytpgllgngneiqrdpgyprdlmppedla 256

Qy 209 -----IYKDCSDYYAIGKRSSSTYRVTDPKPKNSFEVYCDMETMGG 249

Db 257 tsptkspfkippvtfinepfkdcqakeaghsvsgiymlkpenngpmqlwcnslldpg 316

Qy 250 GWTVLQARLDGSTNFTRTWQDYKAGFNLRRFNLGNDKIHLLTKSKEMILRLIDLEDFNG 309

Db 317 gwtvlgkrtgdgsvnfrrwnyknkgfngidgwyglglenymisnqndnykllieledwsd 376

Qy 310 VELYALYDOFYVANEFLKYLRLHVGNYNGTAGDALRPNKHYNHDLKFFTPDKNDNDYPSG 369

Db 377 kkvyaeysfrlepeseefyrlrlgtvggnagdsmmw-----hngkqftldrdkdm-ag 430

Qy 370 NCGLYSSGWFFDACLSANLNGKIYH-QKRGV-RNGIFWGTWPGVSEAHPGYKSSFEKE 427

Db 431 ncahfkggwynacahsnlmgvyrghyrskhgqdgifwaeyrg-----gsy--slra 482

Qy 428 AKMMIRP 434

Db 483 vqmmikp 489

RESULT 15

Y69483

ID Y69483 standard; Protein; 491 AA.

XX Y69483;

XX Y69483;

DT 03-JUL-2000 (first entry)

XX Amino acid sequence of a human angiopoietin (HANG) polypeptide.

DE Human; angiopoietin; HANG; Incyte Clone 2365223; cardiovascular disorder;

XX

CC

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:36 ; Search time 31.84 Seconds
(without alignments)
936.193 Million cell updates/sec

Title: US-09-442-143-2

Perfect score: 2378

Sequence: 1 MKLANWYLSAVLATYGF.....GYKSSFKRAKMIIRPKHKFP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_66:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	100.0	439	2	I37391
2	1853.5	77.9	432	2	A27447
3	1849.5	77.8	432	2	I36934
4	511.5	21.5	463	2	A38463
5	506.5	21.3	312	2	JN0596
6	484.5	20.4	453	1	FGHUGB
7	480.5	20.2	437	1	FGHUG
8	479.5	20.2	479	2	A25052
9	470	19.8	468	1	FGBOB
10	462	19.4	444	2	S05313
11	461	19.4	491	1	FGHUB
12	456	19.2	438	2	A32670
13	452	19.0	334	2	JC5980
14	451	19.0	866	2	D44234
15	446	18.8	282	2	A35084
16	434.5	18.3	326	2	B47172
17	431	18.1	328	2	A05299
18	428.5	18.0	323	2	A47172
19	428.5	18.0	432	1	FGIMGS
20	423	17.8	326	2	S61517
21	423	17.8	1353	1	JH0675
22	417.5	17.6	1356	2	A45445
23	404	17.0	437	1	FGRTGA
24	404	17.0	445	1	FGRTGB
25	403.5	17.0	220	2	S28170
26	403.5	17.0	417	2	S65944
27	401.5	16.9	4135	2	T42629
28	397.5	16.7	3565	1	A40701
29	396	16.7	2019	1	J01322

tenascin-X - mouse
probable tenascin
tenascin-C - human
tenascin precursor
tenascin precursor
tenascin Y precursor
fibrinogen alpha-I
scabrous locus (sc
scabrous protein p
hypothetical prote
hypothetical prote
hypothetical prote
microfibril-associ
hypothetical prote
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

I37391

fibrinogen-like protein expressed in T lymphocytes (p749) - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I37391; S47273

R:Ruegg, C.; Pytel, R.

Gene 160, 257-262, 1995

A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib

A:Reference number: I37391; MUID:95369700

A:Accession: I37391

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-439 <RES>

A:Cross-references: EMBL:Z36531; NID:G535184; PIDN:CAA85298.1; PID:G535185

A:Note: submitted to the EMBL Data Library, August 1994

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 100.0%; Score 2378; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.8e-157;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLANWYLSAVLATYGFVLVANNETEIKDERAKDVCPVRLSRGKCEAGECPYQVS 60

Db 1 MKLANWYLSAVLATYGFVLVANNETEIKDERAKDVCPVRLSRGKCEAGECPYQVS 60

QY 61 LPPLTIOLPKOFSEIEVFKEVQNLKEIVNSLKKSCQDKLOADDNGDPGRNLLPSTG 120

Db 61 LPPLTIOLPKOFSEIEVFKEVQNLKEIVNSLKKSCQDKLOADDNGDPGRNLLPSTG 120

QY 121 APGVGNRRVRESEVKNLSSELKNAKEEINVLHGLEKLNVMNNIENVDSKVANL 180

Db 121 APGVGNRRVRESEVKNLSSELKNAKEEINVLHGLEKLNVMNNIENVDSKVANL 180

QY 181 TFVYNSLDGKCSKPSQEQIQSRPVQHLIYKDCSDYIAIGKRSETYRVTPDPKNSSEV 240

Db 181 TFVYNSLDGKCSKPSQEQIQSRPVQHLIYKDCSDYIAIGKRSETYRVTPDPKNSSEV 240

QY 241 YCDMETGGGWTVLQARLDGSTNTRTWQDYKAGFNLRRFWLGNQKIHLLTKSEKIL 300

Db 241 YCDMETGGGWTVLQARLDGSTNTRTWQDYKAGFNLRRFWLGNQKIHLLTKSEKIL 300

QY 301 RIDLEDFNGVELYALYDQFYVANEFLKRLHVGNYNGTAGDALRFNKHYNHDLKFFTPD 360

Db 301 RIDLEDFNGVELYALYDQFYVANEFLKRLHVGNYNGTAGDALRFNKHYNHDLKFFTPD 360

QY 361 KNDPRYSGNCGLYYSGWFWFACLSANLNGKYYHQYRGVNRGIFWGTWPGVSEAHFPGG 420

Db 361 KNDPRYSGNCGLYYSGWFWFACLSANLNGKYYHQYRGVNRGIFWGTWPGVSEAHFPGG 420

QY 421 YKSSFKKAKMIRPKFKP 439
Db 421 YKSSFKKAKMIRPKFKP 439

RESULT 2
A27447

cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447
R:Toyama, T.; Hall, L.R.; Hasegawa, W.G.; Toneyawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:87175527
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <K>
A:Cross-references: GB:M16238; NID:g103304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 77.98; Score 1853.5; DB 2; Length 432;
Best Local Similarity 77.78; Pred. No. 5.6e-121;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;
QY 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDASQAACPARLESGRC-EGSQCPFLT 58
Db 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDASQAACPARLESGRC-EGSQCPFLT 58
QY 61 LPPLTIQLPKQFSRIEVEFKVQNLKEIVNSLKKSCQDCCKLQADDHDPGGNG---GNG 114
Db 59 LPPLTIQLPKQFSRIEVEFKVQNLKEIVNSLKKSCQDCCKLQADDHDPGGNG---GNG 114
QY 121 APGEVGNRVRELSSEVKNLSSELKNAKEEINVLHGRLEKLNLMNNTIENYVDKAVNL 180
Db 115 AE-TAEDSRVQLESEVKNLSSELKNAKEEINVLHGRLEKLNLMNNTIENYVDKAVNL 180
QY 181 TFVNSLDGKCKSPQSOQIQRVQHLIYKDCSDYIAIGKRSETYRTPDPKNSSEFV 240
Db 174 TVVNSLDGKCKSPQSOQIQRVQHLIYKDCSDYIAIGKRSETYRTPDPKNSSEFV 233
QY 241 YCDMETMGCGTTLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMIL 300
Db 234 YCDMETMGCGTTLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMIL 293
QY 301 RIDLEDFNGVLYALYDQFYVANEFLKYLRLHVGNYNTAGDALRKNKYNHDLKFTTTPD 360
Db 294 RIDLEDFNGVLYALYDQFYVANEFLKYLRLHVGNYNTAGDALRKNKYNHDLKFTTTPD 353
QY 361 KDNDRYPGNGCLYSSGWMFDCSLANLNGKYHOKYKVRNGIFWGTWPGVSEAHPGG 420
Db 354 RNDRYPGNGCLYSSGWMFDCSLANLNGKYHOKYKVRNGIFWGTWPGVSEAHPGG 413
QY 421 YKSSFKKAKMIRPKFKP 439
Db 414 YKSSFKKAKMIRPKFKP 432

RESULT 3
I56934

fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induced
A:Reference number: I56934; MUID:95333285
A:Accession: I56934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-432 <R>
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics:
A:Gene: musfiblp
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 77.88; Score 1849.5; DB 2; Length 432;
Best Local Similarity 77.48; Pred. No. 1.1e-120;
Matches 340; Conservative 42; Mismatches 50; Indels 7; Gaps 4;
QY 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDASQAACPARLESGRC-EGSQCPFLT 58
Db 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDASQAACPARLESGRC-EGSQCPFLT 58
QY 61 LPPLTIQLPKQFSRIEVEFKVQNLKEIVNSLKKSCQDCCKLQADDHDPGGNG---GNG 114
Db 59 LPPLTIQLPKQFSRIEVEFKVQNLKEIVNSLKKSCQDCCKLQADDHDPGGNG---GNG 114
QY 121 APGEVGNRVRELSSEVKNLSSELKNAKEEINVLHGRLEKLNLMNNTIENYVDKAVNL 180
Db 115 AE-TAEDSRVQLESEVKNLSSELKNAKEEINVLHGRLEKLNLMNNTIENYVDKAVNL 180
QY 181 TFVNSLDGKCKSPQSOQIQRVQHLIYKDCSDYIAIGKRSETYRTPDPKNSSEFV 240
Db 174 TVVNSLDGKCKSPQSOQIQRVQHLIYKDCSDYIAIGKRSETYRTPDPKNSSEFV 233
QY 241 YCDMETMGCGTTLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMIL 300
Db 234 YCDMETMGCGTTLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLLTKSKEMIL 293
QY 301 RIDLEDFNGVLYALYDQFYVANEFLKYLRLHVGNYNTAGDALRKNKYNHDLKFTTTPD 360
Db 294 RIDLEDFNGVLYALYDQFYVANEFLKYLRLHVGNYNTAGDALRKNKYNHDLKFTTTPD 353
QY 361 KDNDRYPGNGCLYSSGWMFDCSLANLNGKYHOKYKVRNGIFWGTWPGVSEAHPGG 420
Db 354 RNDRYPGNGCLYSSGWMFDCSLANLNGKYHOKYKVRNGIFWGTWPGVSEAHPGG 413
QY 421 YKSSFKKAKMIRPKFKP 439
Db 414 YKSSFKKAKMIRPKFKP 432

RESULT 4
A38463

fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
C:Accession: A38463
R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745
A:Accession: A38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 21.58; Score 511.5; DB 2; Length 463;
Best Local Similarity 30.48; Pred. No. 5.2e-28;
Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;
QY 31 KDRKRDVCPVRLSEKGC-----EEAGE-CPYQVSLPPLIQLPKQFSRIEVEFKVQNL 84
Db 51 QDKQAMKGPITYPDAGGCKHPLDELGLVLCPTGCE---LQTTLLKQEKTKVPLRLDLKDR 107

```
QY 85 -----LKEIVNSLKSCQCKLQADDNGDGRNGLLPSTGAPGEVGDNRVRELE 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 VAKESDSTTTMYQVNNIDNKLKVKTKQKQK-----NDIILSEYNTMELHYNVIK--D 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 135 SEVKNLSSELKNAKEEINVLHGRLEKLNLMNNNIENYVDSKVNLTFFVNSLDGCKSC 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 NLDNHPSSRLVRAVDSLHKIKOKL-----ENAIATQT-----DYCRSPC 201
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 195 PSQBIQSRPQVLIYKDCSYAIGKRSSSETRYVTPDPKNSSPFVYCDMETMGGGWTVL 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 -----VASCNIPVVSGRECDIYKGGTSEMYIIQDPFTTPPYVYCDMETDNGGWILI 256
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 QARLDGSTNFTRTWQDYKAGGNLRR-----EFWLGNDKIHLLTKSKEMILRID 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 QNRQDGSVNFGRAMDVKYGRGNIAKSGGKYYCDTPGGEVWLGNDKISQLTGKTPKVLIE 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 304 LEDFNGVELYALYDQFYVANEFLKRLHVGNNGTAGDALR--FNKHYN-----HDLK 354
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 317 MEDWNGDKVSALYGGFTIHNEGKYLQSVSNYKGNAGNALMEGASQLYGENRTMTIHNGM 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 FFTPTDKNDRY-----PSGNGCLYSSGWFFDACLSANLNGKYY-----HOKYRGVYN 403
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 377 YFSTYDRNDGWLTTDRPKQCKSKEDGGGWYNRCHAAPNGRYTWGGTYSWDMAKHGTTDD 436
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 404 GIFWGTWPGVSEAHPPGGYKSSFKKAKMIRP 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 437 GIVVMNKG-----SWY--SMKKMSMKIKP 459
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
JN0596
fibrinogen-related protein HFREP-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
Y:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related ge
A:Reference number: JN0596; MUID:93290661
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <YAM>
A:Cross-references: GB:D14446; NID:g933314; PIDN:BAA03336.1; PID:g9393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFREP-1 #status predicted <MAT>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 21.3%; Score 506.5; DB 2; Length 312;
Best Local Similarity 36.8%; Pred. No. 6.8e-28;
Matches 118; Conservative 38; Mismatches 108; Indels 57; Gaps 9;

QY 129 RVRESEVKNLSSELKNAKEEINVLHGRLEKLNLMNNNIENYVDSKVNLTFFVNSLD 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 QVRLLETRVQKQKIKQLLQEE-----NEVQFLDKGDEDTVVD----- 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 GKSKCPSQBIQSRPQVLIYKDCSYAIGKRSSSETRYVTPDPKNSSPFVYCDMETMG 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 -----LGSKRP-----YADCSIFNDGYKLSGFYKIKPKLQSPAEFSVYCDMSD-G 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 GGWTVLQARLDGSTNFTRTWQDYKAGGNL---RREFWLGNDKIHLLTKSKEMILRIDLE 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 GGWTVIQRSDGSFENFRGKDYENGFGNFVQKHGEVWLGKLNHLFTTQEDYTLKIDLA 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 DFNQVELYALYDQFYVANEFLKRLHVGNNGTAGDALRFNKH-----YHDLKFFTTTP 359
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 DFEKSNRYAQYKFNKFGDEKNFELNLTGEYSGTAGDSLGNLHFPHEVQWASHQRMKFSTW 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 DKDNDYPSGNCGLYSSGWFFDACLSANLNGKYYHOKYRG--VRNGIFWGTWPGVSEAH 418
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 DRDHDNY--EGNCAEEDSGHWFNRCHSANLNGVYSGPYAKTDNGIVWYTW----- 288
```

QY 419 GGYKSSFKKAKMIRPKHFKP 439

I: | | | | | | | |

Db 289 HGWWSLKSVVMKIRPNDFIP 309

RESULT 6

FGHUGB

N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain

C:Species: Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999

C:Accession: A90494; A90453; A28203; B28203; I37390; A03126

R:Rixon, M.W.; Chung, D.W.; Davie, E.W.

Biochemistry 24, 2077-2086, 1985

A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.

A:Reference number: A90494; MUID:85252774

A:Accession: A90494

A:Molecule type: DNA

A:Residues: 1-113, 'I', 115-453 <RIX>

A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:gl82438; PIDN:AAB

R:Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.

J. Biol. Chem. 259, 12826-12830, 1984

A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t

A:Reference number: A92448; MUID:85030379

A:Accession: A92448

A:Molecule type: DNA

A:Residues: 286-453 <FOR>

R:Wolfenstein-Todel, C.; Mosesson, M.W.

Biochemistry 20, 6146-6149, 1981

A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain varia

A:Reference number: A90453; MUID:82068993

A:Accession: A90453

A:Molecule type: protein

A:Residues: 411-434, 'Y', 436-440, 'Z', 442, 'Z', 444, 'B', 446-447, 'R', 449, 'ZBB', 453 <WOL>

R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.

Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988

A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-cha

A:Reference number: A94194; MUID:88217900

A:Accession: A28203

A:Molecule type: protein

A:Residues: 433-449 <FRA>

A:Accession: B28203

A:Molecule type: protein

A:Residues: 433-453 <PR2>

R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.

DNA Seq. 1, 419-422, 1991

A:Title: Polymorphism of the human gamma chain fibrinogen gene.

A:Reference number: I37390; MUID:92119334

A:Accession: I37390

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 75-286 <RES>

C:Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064

C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate

ntron, which makes this chain different from the gamma-B chain at positions 434-437 a

C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in p

C:Genetics:

A:Gene: GDB:FGG

A:Cross-references: GDB:119132; OMIM:134850

A:Map position: 4q28-4q28

A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1

C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR

ins are contained in the core. Two three-chain coiled coils emerge from this core and

from the distal domain nodes.

C:Function:

A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in

A:Pathway: blood coagulation

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote

F:1-36/Domain: signal sequence #status predicted <SIG>

F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>

F:176-415/Domain: fibrinogen beta/gamma homology <FBG>

F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization #status, binding to the amino end of the alpha chain of an
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:49/Disulfide bonds: interchain (to alpha-64) #status predicted
F:78/Binding site: carboxylate (Asn) (covalent) #status predicted
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status predicted

Query Match 20.4%; Score 484.5; DB 1; Length 453;
Best Local Similarity 29.7%; Pred. No. 3.8e-26;
Matches 141; Conservative 56; Mismatches 178; Indels 99; Gaps 18;

Qy 8 WLSSAVLATYGLVANNETEIKDERAKDVCVRLESRGKCEACECPYQVSLPPLTIQ 67
Db 19 FLSSFCVA-----YVATRDNCCLILDERFGSYCPT-----TCGIADFLSYQTK 61
Qy 68 LPKQPSRTEVEFEQVNLKIEVNSLKKSCQCKLQADDDGDPGRNGLLLPSTGAPCEVGD 127
Db 62 VDKDLQSLIEDILHVENKTSEVKQLIKAIQ-LTYNPDESCKPMI-----DAAT 109
Qy 128 NRVRESEVNKLSELKNAKEEINVLHGRLEKLNIVNNNIENYVDSKVANLTFVNSL 187
Db 110 LKSRKMLEEIMKYEASILTHDSIRYLQ-----EIYNSNN-----QKIVNLKQVAQL 157
Qy 198 DGKCKSPQEOIQSPVQHLIYKCSDYIATGKRSEYRYVTPDPKNSFEVCDMETM 247
Db 158 EAQCOE-PCKDTVQ---IHDTGKCDQITANKGAKOSGLYFKPLKANOQFLVYCEIDGS 213
Qy 248 GGGWTVLQARLDSTNFTWQDYKAGFNL---RREFWLGNDKIHLLTKSEM--ILR 301
Db 214 GNGWTVFKRLDGSVDFKKNWLOYKEGFGHLSPGTGTFWLGNKELHLSITQSAIPALR 273
Qy 302 IDLEDFNGVELYALDQFVAVNEFLKRYLHVGNV-NGTAGDAL-RFNKYNHDLKFFT-- 357
Db 274 VELEDWNGRTSTADYAMFKVGPPEADKRYLYAYFAGDAGDAFDGDFGDDPSDKFTSH 333
Qy 358 -----TPDKNDNRVPSGNCGLYYSGWFWFDACLSANLNGKYH-----QKRYGVNRG 404
Db 334 NGMQPSTWDDNDKF-EGNCAEODGSGGWMNCKHAGLNGVYQGGTYSKASTPNGYDNG 392
Qy 405 IFWGTWP-----GVSEA---HPGGYKSSFEAKMMIRPKH 436
Db 393 IIVATWTKRWYSMKKTKMIIPNRLTIGEGQOHLGGAK-----QVRPEH 438

RESULT 7
FCHUG
fibrinogen gamma-A chain precursor - human
N:Alternate names: coagulation factor I
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 25-Feb-1985 #text change 21-Jul-2000
C:Accession: A90470; B90494; C94433; B93956; B92448; 137393; A40698; H54223; A03125; C37
R:Chung, D.W.; Chan, W.Y.; Davie, E.W.
Biochemistry 22, 3250-3256, 1983
A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
A:Reference number: A90470; MUID:83283434
A:Accession: A90470
A:Molecule type: mRNA
A:Residues: 1-437 <CHU>
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: B90494
A:Molecule type: DNA
A:Residues: 1-113, '1', 115-437 <RIX>
A:Cross-references: GB:X02415; GB:M10014; NID:g182436; PIDN:AAB59531.1; PID:g182439

R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peters, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structure
A:Reference number: A94433
A:Accession: C94433
A:Molecule type: protein
A:Residues: 27-437 <HEN>
R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A:Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains:
A:Reference number: A93956; MUID:83247396
A:Accession: B93956
A:Molecule type: mRNA
A:Residues: 276-437 <KAN>
R:Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
A:Reference number: A92448; MUID:85030379
A:Accession: B92448
A:Molecule type: DNA
A:Residues: 286-437 <FOR>
R:Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A:Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chai
A:Reference number: 137393; MUID:84069777
A:Accession: 137393
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 209-270 <RES>
A:Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:g577055
R:Bertagnoli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with
A:Reference number: A40698; MUID:93286185
A:Accession: A40698
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <BER>
A:Experimental source: thrombin-activated platelets
A:Note: sequence extracted from NCBI backbone (NCBIP:133734)
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A:Reference number: A54223; MUID:94162201
A:Accession: H54223
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <KUN>
A:Note: identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370
A:Contents: annotation; review, disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080
A:Contents: annotation; disulfide bonds
R:Hoepflich, P.D.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1983
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bond
A:Reference number: A90467; MUID:83231465
A:Contents: annotation; quaternary structure, disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Horwitz, B.H.; Varadi, A.; Scheraga, H.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A:Reference number: A94006; MUID:85014892
A:Contents: annotation; polymerization region
R:Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-1774, 1984
A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure
A:Reference number: A90483; MUID:84203545
A:Contents: annotation; platelet aggregation region
R:Plow, E.F.; Srouji, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.
J. Biol. Chem. 259, 5388-5391, 1984
A:Title: Evidence that three adhesive proteins interact with a common recognition site
A:Reference number: A92477; MUID:84185664
A:Contents: annotation; platelet aggregation region
R:Dang, C.V.; Ebert, R.F.; Bell, W.R.
J. Biol. Chem. 260, 9713-9719, 1985
A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit positions
A:Reference number: A92549; MUID:85261382
A:Contents: annotation; calcium binding region
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-terminus
A:Reference number: A37117; MUID:90337977
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemophilia ghiliani, the giant South American leech,
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilizing
gel) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate splicing
intron, which makes this chain different from the gamma-B chain at positions 434-437 and
C:Genetics:
A:Gene: GDB:FCG
A:Cross-references: GDB:110132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGHUGB)
ins are contained in the core. Two three-chain coiled coils emerge from this core and coiled
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of an
F:423-437/Region: platelet aggregation #status predicted
F:34/Disulfide bonds: interchain (to gamma-35) #status experimental
F:35/Disulfide bonds: interchain (to gamma-34) #status experimental
F:45/Disulfide bonds: interchain (to beta-110) #status experimental
F:49/Disulfide bonds: interchain (to alpha-64) #status experimental
F:78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:161/Disulfide bonds: interchain (to beta-227) #status experimental
F:169/Disulfide bonds: interchain (to alpha-180) #status experimental
F:175/Disulfide bonds: interchain (to alpha-180) #status experimental
F:424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status experimental
F:432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status experimental

Query Match 20.2%; Score 480.5; DB 1; Length 437;
Best Local Similarity 31.2%; Pred. No. 6.8e-26;
Matches 133; Conservative 53; Mismatches 171; Indels 69; Gaps 15;
QY 8 WLSSAVLATYGLVWANNTEETKDEKADKCPVRLSRGKCEGCEPCQVSLPPLTIQ 67
DB 19 FLUSSTCVA-----YVATRDNCCLILDERFGSYCPT-----TCGIADFLSTYQTK 61
QY 68 LPKQFSRIEVEFVONLKEIVNSLKSCDCKLQADDNGDPGRNGLLLPSTGAPGEVD 127

Db 62 VKDKLQSLIEDILHQVENKTSYEVKQLIKATQ-LTYNPDESSKPNMI-----DAAT 109
QY 128 NRVRELESEVNNLSLSSKLNKAKEINVLHGRLEKLNLVNMMNIENYVDSKVANLTFVYVNSL 187
Db 110 LKSRKMLEIMYEASILTHDSIRVLQ-----EYNSNN-----QKIVNLKEVAQL 157
QY 188 DGKCKSPQEQIQSRPVQHLIYKDCSDYYAIGKRSEYRVTDPKNSSEFVYCDMETM 247
Db 158 EAQCQE-PCKDRVQ---IHITGKDCQDIANKGAKQSGLYFIKPLKANOQFLVYCEIDGS 213
QY 248 GGGWTVQLARLDGSGNFTFTWQDYKAGFNL----RREFWLGNDKIHLITKSKEM--ILR 301
Db 214 GNGWTFQKRLDGSVDKKNWYQYKEGFGHLSPGTFTFWLGNKIHLLISTQSAIPYALR 273
QY 302 IDLEDFNGVELYALYDQFVYVANEFLKYRLHVGNY-NGTAGDAL-RENNKHVHDLKKEFT-- 357
Db 274 VELEDWNGRTSTADYAMFVKVGEADKYRTYAYFAGGDAGDAPDGFDDPSDKKEFTSH 333
QY 358 -----TPDKDNDRYPSGNGCLYSSGWWFDCLSANLNGKYYH-----QKRYGVRNG 404
Db 334 NGCMQSTWDNDKFP-EGNCAEQDGGSGWMMKCHAGLNGVYVYOGGTYSKASTPPNGYDNG 392
QY 405 IFWGTW 410
Db 393 LIWATW 398
RESULT 8
fibrinogen beta chain - sea lamprey (fragments)
N:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <GB>
A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
R:Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A:Reference number: A03120; MUID:77065679
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu-
C:Keywords: blood coagulation; glycoprotein; sulfoprotein
F:1-36/Product: fibrinopeptide B #status experimental <FPB>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:90-219/Domain: fibrinogen disulfide ring homology <FDR>
F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.2%; Score 479.5; DB 2; Length 479;
Best Local Similarity 29.2%; Pred. No. 9e-26;
Matches 131; Conservative 66; Mismatches 138; Indels 113; Gaps 15;

QY 29 ELKDERAKDPCVRLSRGKCEGCEPCQVSLPPLTIQPKQFSRIEVEFVONLKEI 88
Db 102 ELREELLKORDPVR-----YKISMLK-----QNLATYF 128
QY 89 VNSLKSCDCKLQADDNGDPGRNGLLLPSTGAPGEVGNRVRELESEVNSLKSSLSLNAK 148
Db 129 INSDFR-----MASDSNTLKQN-----VQTLRRRLNSRSTHVAQ 164

F; 215-464/Domain: fibrinogen beta/gamma homology <FBG>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 6/Binding site: sulfate (Tyr) (covalent) #status experimental
F; 21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F; 371/Binding site: carbonylate (Asn) (covalent) #status predicted
F; 372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 19.8%; Score 470; DB 1; Length 468;
Best Local Similarity 30.6%; Pred. No. 4e-25;
Matches 129; Conservative 57; Mismatches 149; Indels 86; Gaps 13;

	QY	61	LPPLTIOLPKQFSRIEE-VKEQEONLKEIVNSLKSKQCDC--KLQADDNGDPCRNGLLLP 117
		: :	: :: ::
Db	82	LCPTGCCKLODTLVQRQERPIRKSIEDLRNTVDVSRTSSSTFYITILKKNMKGR----- 135	
		: :: :: :: :	:
QY	118	STGAPEVGDNRVRELESEVYNKLSSELKNAAKEINVHLHGLEKLNLMNMNIENIYDSKV 177	
		: :: :: :: :	: :: :: :: :
Db	136	-----QNQODNENVNVYEISS-----HLEKHQLYIDETVKNNIPTKL 172	
		: :: :: :: :	:
QY	178	ANLTFFVNISLDGKCSKPCEIQISR-----PVQHLYIKDCSDYYAIGKRSES 225	
		: :: :: :: :	: :: :: :
Db	173	RVLRSILENLRSKIQLKESDVSTQMEXCRTPCTVTNCIPV--VSGKECEKIIRNEGETSE 230	
		: :: :: :: :	: :: :: :
QY	226	TYRVPDPKNSFEVCMDMETMGGWTVLQARLDGSTNFTRTWODYKAAGFNLR----- 280	
		: :: :: :: :	: :: :: :: :
Db	231	MILIQPDESPPKYRYCDMKTGGWTFVIQNRDGSLDFGKKWDPKQGFGNTATNAEGK 290	
		: :: :: :: :	:
QY	281	-----EFWLGNDKIHLLTKSEMILLRIDLFPGVELVALYDOVFVAEFLKYRLHVGS 333	
		: :: :: :: :	: :: :: :: :
Db	291	KYCVPGEYLWNDRITSOLSINRMGTULLIEDMDWKGDVTLALYEGFTVQAANKYQLSVS 350	
		: :: :: :: :	: :: :: :: :
QY	334	NYGTTAGDAL-----RFNKHYN-HDLKFTHFPKDNDRY----PSGNCGLYYSSGMW 380	
		: :: :: :: :	: :: :: :: :
Db	351	KYKGTAGNALIEGASQLGVENRWTFIHNSMFSTYDEDDNGKWTTDPKOCCKEDGGWW 410	
		: :: :: :: :	: :: :: :: :
QY	381	FDACLSANLGKXY-----HOKRGVRNGIFWGTPGVSEAHPGGYKSSFKEAKMMIR 433	
		: :: :: :: :	: :: :: :: :
Db	411	YNRCHAAMPNGRYWGAYTWMADKHTDGDGVVMNQO-----SWY---SMKKMSMKIR 462	
		: :: :: :: :	: :: :: :: :
QY	434	P 434	
Db	463	P 463	

RESULT 10
S05313
fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: S05313
R:BROWN, W.M.; Dieglelewski, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A>Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinogen
A:Reference number: S05313; PMID:89366676
A:Accession: S05313
A:Molecule type: mRNA
A:Residues: 1-444

A:CROSS-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350
A>Note: The authors translated the codon AGT for residue 105 as Ala and ATT for resid C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-444/Product: fibrinogen gamma-B chain #status predicted <NAT>
F; 174-414/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.4%; Score 462; DB 2; Length 444;
Best Local Similarity 30.5%; Pred. No. 1.3e-24;
Matches 142; Conservative 51; Mismatches 164; Indels 108; Gaps 19;

Qy	9	LSSAVLATYGFVLVVANNETEIKDERAKDVCYPVKSRRGKCERAGECPYOVSPLPTIQL 68
		: :: :: :: :
Db	18	LSSACL A-----YVATRDNCCILDREFGYSCPT-----TCGIADFLLNNYTQTSV 60
		: :: :: :: :

R; Watt, K.W.K.; Takegi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; MUID:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R;Blomback, B.; Hessel, B.; Hoger, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080
A:Contents: disulfide bonds
A:Accession: A94309
A:Molecule type: protein
A:Residues: 31-112, 'B', 114-137, 'QS', 140-144, 'QF', 147-148 <BLO>
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.;
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
A:Reference number: A54223; MUID:94162201
A:Accession: G54223
A:Molecule type: protein
A:Residues: 164-174 <KUN>
A:Note: identification of tryptic peptides from high-density lipoproteins
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370
A:Contents: annotation; review; disulfide bonds
R;Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
A:Reference number: A91249; MUID:77245999
A:Contents: annotation; disulfide bonds
R;Doolittle, R.F.; Takegi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.;
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F.
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751
A:Contents: annotation; review, EM structure, polymerization, ligands
R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA.
A:Reference number: A90038; MUID:83254384
A:Contents: annotation
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH
A:Reference number: A37117; MUID:90337977
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemateria ghilianii, the giant South American leech
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilizer)
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FCB
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-4q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR) and
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic
F:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>

F:31-491/Product: fibrinogen beta chain #status experimental <MAT>
F:31-44/Product: fibrinopeptide B #status experimental <APT>
F:45-491/Product: fibrin beta chain #status experimental <RGB>
F:45-47/Region: polymerization site
F:99-228/Domain: fibrinogen disulfide ring homology <FDR>
F:238-487/Domain: fibrinogen beta/gamma homology <FBG>
F:31/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental
F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
F:95/Disulfide bonds: interchain (to alpha-55) #status experimental
F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:231-316,241-270,424-437/Disulfide bonds: #status experimental
F:394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 461; DB 1; Length 491;
Best Local Similarity 28.7%; Pred. No. 1.8e-24;
Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps 14;

Qy 27 TEELDERAKDVCVRLESRGKEAGE-----CPYQVSLPLTLTQLPKQF-SRIEEVEK 80
Db 81 TQKKVERAPDA-----GCGLHADPLGLVLCPTGCGQLQALQOERPIRNSVDELNN 132
Qy 81 EVONLKEIVNS-----LKKSCDCKLQADNGDGPGRNGLLPLSTGAPGEVDNRVREL 133
Db 133 NVEAVSQTSSSSFQMYLLKDLQKQKQKQKDN----- 165
Qy 134 ESEYNKLSSELKNAKEEINVLHGRLEKLNLMNMIENYVDSKVANLTFVNSLDGCKSK 193
Db 166 ENVNVEYSSE-----LEKHQLYIDETVNSNIPNLRVLRILENLSKIQK 211
Qy 194 CPSQBIQ-----SRPVOHLIYKDCSDYAIAGKRSSSTYRTPDPKNSRFEVYCD 243
Db 212 LESDVSADMEYCRTPCTVSCNIPVVSGRKECEIIRKGGTSEMYLIQPDSSVKPYRYCD 271
Qy 244 METGGGVTVLQARLDGSTNFTRTWDYKAGFGN-----LRREFWLGNDKRIHL 291
Db 272 MNTENGWTVIQNRQDGSDFGRKKDPYKQGFGNATNDGKNYCOLPGEYWLGNDKISQ 331
Qy 292 LTKSKEMILRDLDFNGVELYALYDQFVANEFLYRLHVGNYNTAGDALR----- 344
Db 332 LTRMGPTLELLEMDKGDVKAHYGGFTVQNEANKYQISVKNYRGTAGNALMDGASQLM 391
Qy 345 -FNKHYN-HDLKFFFTDPKNDRY----PSGNCGLYSSGWFWFDACLSANLNGKY- 394
Db 392 GENRTWTHNGMFFSTYDRKNDGWLTSDDPKQCKEDGGGWYNRCHAANPNGRYTWGGQ 451
Qy 395 ---HOKYRGVNRGIFWGTWPGVSEAHPGGYKSSFKAKMIRP 434
Db 452 YTDWMAKHGTDGQVVMWVWKG-----SWY--SMRKMVMKIRP 486

RESULT 12
A32670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; MUID:90241882
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02894; NID:q214139; PIDN:AAA49709.1; PID:q214140
P:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of xenopus
A:Reference number: I51416; MUID:91146806

A:Accession: I51416
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-58 <BHA>
A:Cross-references: GB:M35548; NID:q214141; PIDN:AAA03247.1; PID:q214142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.2%; Score 456; DB 2; Length 438;
Best Local Similarity 30.4%; Pred. No. 3.4e-24;
Matches 130; Conservative 69; Mismatches 158; Indels 70; Gaps 17;

Qy 10 SSAVLATYGLVYANNETEIRKADKVCVRLESRGKEAGECPYQVSLPLTLTQLP 69
Db 14 SLALLSSAFGNIIPNTDNCCLDGRFGEYCPT-----TCGIS 50
Qy 70 KQFSRIEE-VFKEVQNLKEIVNSLKKSCDCKLQADNGDGPGRNGLLPLSTGAPGEVGDN 128
Db 51 DFLNRYQENVDTDLQYLENLLTQISNISTGTTIIVEHLIDSGKKPATSPQTAI-----DP 105
Qy 129 RVRELESEYNKLSSELKNAKE-EINVLHGRLEKLNLMNMIENYVDSKVANLTFVNSL 187
Db 106 MTKSTCTWKKL-TDMKNYYQYEEIILY--LQEVYSSNQNKI-FLKKOKIANLEL----- 156
Qy 188 DGRCKSCPSEQIQSRPVOHLIYKDCSDYAIAGKRSSSTYRTPDPKNSRFEVYCDMETM 247
Db 157 --QCQO-PCRDVTQ---IQEFTGKDCQEVANKGARGSLYIKPLKAKQOFLVYCEIEPS 210
Qy 248 GGWTVLQARLDGSTNFTRTWDYKAGFG-----NLRREFWLGNDKRIHLTKSKEM--ILR 301
Db 211 GSAWTVIQRRLDGSVNFHKNWQVREGFYLSPLNDKTEFWLGNKEIHLSTQSTIPYVMR 270
Qy 302 IDLEDFNGVELYALYDQFVANEFLYRLHVGNY-NTAGDAL-----RFNKHV-NH 351
Db 271 IELEDSNQSSTADYSTFRLGSEKDNRYFTYAYFIDGADGDAFDGDFDGDPSDKFTSH 330
Qy 352 DLKFFFTDPKNDRYPSGNCGLYSSGWFWFDACLSANLNGKYH-----OKYRGVRN 403
Db 331 NGQWQSTFDKNDKF-DGCAEODGSGWNNRCHAHLNGKYOGGTYSEADSPSGVDN 389
Qy 404 GIFWGTW 410
Db 390 GIWATW 396

RESULT 13
JC5980
ficollin-A precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000
C:Accession: JC5980
R:Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachikawa, H.; F
Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A:Title: Molecular cloning and characterization of mouse ficollin-A.
A:Reference number: JC5980; MUID:98205801
A:Accession: JC5980
A:Molecule type: mRNA
A:Residues: 1-334 <FUJ>
A:Cross-references: DDBJ:AB007813; NID:g2957011; PIDN:BAA25126.1; PID:d1026054; PID:g
A:Experimental source: liver
C:Comment: This protein consists of both collagen- and fibrinogen- like domains.
C:Superfamily: fibrinogen beta/gamma homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:50-64,68-106/Domain: collagen-like #status predicted <COL>
F:123-334/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.0%; Score 452; DB 2; Length 334;
Best Local Similarity 34.4%; Pred. No. 4.4e-24;
Matches 114; Conservative 35; Mismatches 106; Indels 76; Gaps 12;


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Qy 211 KDCSDYY--AIGKR-SSETYRVTPDPKNSFEVYCDMETMGGWTVLQARLDGSTNFTRT 267
Db :||| | : | | | : || | : || || | || | | : || | : || | :
68 RDCYDILQSCSQSPSGYYIQPDGNN-LIKVYCDMETDEGWTVFQRRIDCTINFYRS 126
Qy 268 WQDYKAGFGNLRREFWLGNDKIHLTKSEMLLRIDLEDFNGVELYALYDOFYVANEFLK 327
Db | : || || | || || || | : || : | : | | : | : | : | :
127 WSYTQTGFENLTFEFLGNDNIHYLTSGDYELRVELNNTLGNHYYAKYKFRIGDSFSE 186
Qy 328 YRLHVGNYNGTAGDALRFNKHYNHDLKFPTTDPKDNDRYPSGNCGLYSSG---WWFDAC 384
Db | : | : || || | : | : | : | | | | | | : | | : | | : |
187 YLLVLGAYSGTAGDSLAY-----HNTMRESTDNDNDVY-SINCASHSSYGRCAWYKSC 240
Qy 385 LSNLNGKYHQQYRGVRNGIFWGTWPGVSEAHPGYKSSFKKMMIR 433
Db | : || || : || | | : | : | : | : | : | : | : |
241 LLSNLNGQYY--DYSGAPS-IYWSYLPGDNDQIP-----FAEMKLRNR 280
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Search completed: February 27, 2001, 12:50:10
Job time: 154 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:34 ; Search time 21.07 Seconds
(without alignments)
374.141 Million cell updates/sec

Title: US-09-442-143-2

Perfect score: 2378

Sequence: 1 MCLANWYWLSSAVLATYGL.....GYKSSFKEAKMIRPKHFKP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2.6/ptodata/2/iaa/6_COMB.pep.*
 - 4: /cgn2.6/ptodata/2/iaa/PCRUS_COMB.pep.*
 - 5: /cgn2.6/ptodata/2/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	524	22.0	314	1	US-08-525-505A-2
2	522	22.0	496	1	US-08-373-579-6
3	522	22.0	496	2	US-08-418-595-6
4	522	22.0	496	2	US-08-665-926-6
5	522	22.0	496	3	US-09-162-437-6
6	506.5	21.3	286	3	US-08-960-507-20
7	506	21.3	312	1	US-08-525-505A-4
8	505	21.2	491	3	US-08-933-821-4
9	505	21.2	491	3	US-08-960-507-4
10	489	20.6	346	3	US-08-960-507-19
11	487	20.5	497	1	US-08-373-579-4
12	487	20.5	497	2	US-08-418-595-4
13	487	20.5	497	2	US-08-665-926-4
14	487	20.5	497	2	US-08-348-492-4
15	487	20.5	497	3	US-09-162-437-4
16	481.5	20.2	453	1	US-08-206-176-6
17	480.5	20.2	493	2	US-08-933-821-2
18	480.5	20.2	493	3	US-08-960-507-2
19	480.5	20.2	498	3	US-08-373-579-2
20	480.5	20.2	498	2	US-08-418-595-2
21	480.5	20.2	498	2	US-08-665-926-2
22	480.5	20.2	498	2	US-08-348-492-2
23	480.5	20.2	498	3	US-09-162-437-2
24	468	19.7	411	1	US-08-232-532-1
25	468	19.7	411	2	US-08-748-150-1
26	468	19.7	411	4	PCT-US95-05168-1
27	467.5	19.7	509	2	US-08-665-926-8
28	461	19.4	491	1	US-08-206-176-4
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					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 4, Appli
					Sequence 4, Appli
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					Sequence 19, Appl
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					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 4, Appli

29	458.5	19.3	454	3	US-08-434-099A-27	Sequence 27, Appli
30	458.5	19.3	454	3	US-08-434-099A-28	Sequence 28, Appli
31	446	18.8	282	3	US-08-812-586-49	Sequence 49, Appli
32	444	18.7	214	3	US-08-960-507-21	Sequence 21, Appli
33	439.5	18.5	236	3	US-08-886-269-2	Sequence 2, Appli
34	439.5	18.5	236	3	US-09-167-647-2	Sequence 2, Appli
35	439.5	18.5	470	2	US-08-933-821-6	Sequence 6, Appli
36	439.5	18.5	470	2	US-08-960-507-6	Sequence 6, Appli
37	438.5	18.4	236	3	US-08-886-269-1	Sequence 1, Appli
38	438.5	18.4	236	3	US-09-167-647-1	Sequence 1, Appli
39	431.5	18.1	236	3	US-08-886-269-4	Sequence 4, Appli
40	431.5	18.1	236	3	US-09-167-647-5	Sequence 5, Appli
41	429.5	18.1	236	3	US-08-886-269-3	Sequence 3, Appli
42	429.5	18.1	236	3	US-09-167-647-4	Sequence 4, Appli
43	421	17.7	1358	1	US-08-404-665-4	Sequence 4, Appli
44	421	17.7	1358	1	US-08-404-671-4	Sequence 4, Appli
45	421	17.7	1358	1	US-08-404-781-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-525-505A-2
; Sequence 2, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAKO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525.505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-505A-2

Query Match 22.0%; Score 524; DB 1; Length 314;
Best Local Similarity 37.6%; Pred. No. 1.9e-40;
Matches 124; Conservative 46; Mismatches 104; Indels 56; Gaps 13;
QY 125 VGD-NRVE---LESEVKNLSSELKNAKEE-IVLHGRLEKLNLMNMIENYVDSKVAN 179
DB 23 LGDENCLQEQVRLRAQVRLQLETRVQKQVIAQLLHEK--EVQFLDRGOEDSFID----- 75
QY 180 LTFVNVSLDGRKSCPCSQEQIQSRPVQHLIYKDCSDYYAIGKRSTYRTVPDPKNSSFE 239
DB 76 -----LGGK-----RH--YADCEIYDNGFKHSGFYKIKPLQSLAEFS 111
QY 240 VYCDMETGGGWTVLOARLDGNTNTRTWQDYKAGFNL---RRFELGNDKIHLLTKSK 296
DB 112 VYCDMSD--GGGTVTIQRSDGSENFRGNDYENGFGNFVQSGEYWLGNKNINLLTMOG 170
QY 297 EMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNNGTAGDALRENKH-----YN 350
DB 171 DYTILKIDUTDEKNSRFAQYKFKYGDGKSFYELNIGEYSGTAGDSLCTTFHPEVQWNAS 230
QY 351 HDLKEFTTPDKNDPRYSGNGLYYSSGWWFDCALSANLNGKYYHOKYRG--VRNGIFWGT 409
DB 231 HOTMKFSTRDRNDNY--NGNCAEEBQSGWFWNFRCHSANLNGVYYQGPYRAETDNGVWYT 289
QY 410 WPGVSEAHGGYKSKFKEAKMMIRPKHPK 439
DB 290 W-----RGWYSLKSVKMRPSDFP 311

RESULT 2

US-08-373-579-6
; Sequence 6, Application US/08373579
; Patent No. 5650490
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Covert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-373-579-6

Query Match 22.0%; Score 522; DB 1; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LESRGKCE--EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFEVQN 84
DB 26 MDSIGKQYQVHGSCSYTFLLPEMDNCRSSSPYVNAVORDAPLEYDDSVQRLQVLEN 85
QY 85 LKE-----IVNSLKKSCQDCKLQADDNGDGRNGLLLPSTGATGEVGDN---- 128
DB 86 IMENNTQMLKLENYIQDNMKKEMVEIQNAVQN-----QTAVMIEIGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
DB 135 TAEQTRKLTDEAQLVNTQTRLEQLLLEHLSLSTNKLKQILDQTSINKLQDKNSFLEKK 194
QY 162 NLV-----NMNIENYVDSKVANLTF-----V 183
DB 195 VLAMEDKHIIQLOSIKEEKDQLQVLVSKQNSIIIEELEKKIVTATVNSVLQKQOHDLMET 254
QY 184 VNSLDKCKSCPCSQEQIQSRPVQHLIYKDCSDYYAIGKRSTYRTVPDPKNSSFEVYCD 243
DB 255 VNNLLTMMSTNSAKDPTVAKEQISFRDCAEVPKSGHTTNGIYTLTFPNSTEEIKAYCD 314
QY 244 METMGGGWTVLOARLDGNTNTRTWQDYKAGFNLRRFELGNDKIHLLTKSKEMILRID 303
DB 315 MEDAGGGWTTIQRREDGSDVDFQRTWKYKVGFGNPSGEYWLGNFVSQLTNQOQRYVLKH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNNGTAGDALFRNKHYNHDLKFFFTPPDKDN 363
DB 375 LKDWEGNEAIVSLYEHFYLSSLELNRYHLKGLTGTACKISSISQPGND----FSTKGDGN 430
QY 364 DRYPSGNCGLYYSSGWWFDCALSANLNGKYYHOKYRGV-NGIFWGTWPGVSEAHGGYK 422
DB 431 DKCIC-KCSQMLTGGWFWDCAGPSNLNGMYYPQRTNKFNGIKWYWKG-----SGY- 482
QY 423 SSFKEAKMMIRPKHP 437
DB *483 -SLKATTMIRPADF 496

RESULT 3

US-08-418-595-6
; Sequence 6, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595

RESULT 4
US-08-665-926-6
; Sequence 6, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-595-6

Query Match 22.0%; Score 522; DB 2; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Qy 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 MDSICKKQYQVHGSCSYTFLPEMDNCRSSSPYVSNVQADAPLEYDDSVQRLQVLEN 85
Qy 85 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVDN--- 128
Db 86 IMENNTQWLKLENYIQDNMKKEMVEIQONAVN-----QTAVMIEIGTNLLNQ 134
Qy 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
Db 135 TAEQTRKLTDEVAQVNLQTTRELEQLLEHSLSTNKLEKIQILDQTSSEINKLQDKNSFLEKK 194
Qy 162 NLV-----NMNINENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIKEEKDQQLVLSKONSIEELEKKIVTATVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKCKSPQEQIQSRPVQHLIYKDCSDYYAIGKRSSSETYRTPDPKNSSEFVEYCD 243
Db 255 VNNLLTMSTNSAKDPTVAKEEQISFRDCAEVKSGHTNGIYTLTFPNSSTEEIKAYCD 314
Qy 244 METMGCGWTVLQALDQSTNFTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
Db 315 MEAGGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPSGEYWLGNFVSQLTNQOQRYVLKIH 374
Qy 304 LEDFNGVELYALYDOFYVANEFKLYRLHVGNYNGTAGDALRNKHNHDLKFTTPDKON 363
Db 375 LKDWEGNEAYSLEYEHFYLSSSEELNRIHLKGLTGTAGKISSISQPGND-----FSTKQDGN 430
Qy 364 DRYPSCNGCLYSSGWWFDAQLSANLNGYKHYHQYKRGVR-NGIFWGTWPGVSEAHPPGGY 422
Db 431 DKCIC-KCSQMLTGWGFDACGPNLNGMYYPQRQNTKNGIKYWKG-----SGY- 482
Qy 423 SSFKEAKMWIRPKHF 437
Db 483 -SLKATTMMIRPADF 496

Query Match 22.0%; Score 522; DB 2; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
Qy 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 MDSICKKQYQVHGSCSYTFLPEMDNCRSSSPYVSNVQADAPLEYDDSVQRLQVLEN 85
Qy 85 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVDN--- 128
Db 86 IMENNTQWLKLENYIQDNMKKEMVEIQONAVN-----QTAVMIEIGTNLLNQ 134
Qy 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
Db 135 TAEQTRKLTDEVAQVNLQTTRELEQLLEHSLSTNKLEKIQILDQTSSEINKLQDKNSFLEKK 194
Qy 162 NLV-----NMNINENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIKEEKDQQLVLSKONSIEELEKKIVTATVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKCKSPQEQIQSRPVQHLIYKDCSDYYAIGKRSSSETYRTPDPKNSSEFVEYCD 243
Db 255 VNNLLTMSTNSAKDPTVAKEEQISFRDCAEVKSGHTNGIYTLTFPNSSTEEIKAYCD 314
Qy 244 METMGCGWTVLQALDQSTNFTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
Db 315 MEAGGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPSGEYWLGNFVSQLTNQOQRYVLKIH 374
Qy 304 LEDFNGVELYALYDOFYVANEFKLYRLHVGNYNGTAGDALRNKHNHDLKFTTPDKON 363
Db 375 LKDWEGNEAYSLEYEHFYLSSSEELNRIHLKGLTGTAGKISSISQPGND-----FSTKQDGN 430

Query Match 21.3%; Score 506.5; DB 3; Length 286;
Best Local Similarity 36.0%; Pred. No. 6.9e-39;
Matches 112; Conservative 49; Mismatches 121; Indels 29; Gaps 7;
QY 128 NRVRELESEVKNLSSELKNAKEEINVHGRLEKLNLMNMIENIYVDSKVANLFTVNSL 187
DB 4 DQQLVLSKQNSIELEKKIVTAVNSVLQKQOQHDLMETVNNL-----LTMSTSN 56
QY 188 DGRCSKCPQEQIQSRPVQHLIYKDCSDYIAIGKRSETYRVPDPKNSFEVYCDMETM 247
DB 57 SAKDPTVAKEEQIS-----FRDCAEVKSGHTTNGIYTLTPNPSTEIKAYCDMEAG 108
QY 248 GGGWTVLQARLDGSGTFTWQDYKAGFNLRRFEFLGNDKIHLLTKSKEMILRIDLEDF 307
DB 109 GGGWTIIQRREDGSDVQRTWKYKVGFGNPSGEYWLGNFVSQLTNQQRVLIHLKDW 168
QY 308 NGVELYALYDQFVYANEFKYLRLHVGNYNGTAGDALRFNKHNDLHDLFTTTPDKNDRYP 367
DB 169 EGNEAYSLYEHFVLSSEELNYRHLKGLTGTACKISSIQPGND---FSTKGDNDKCI 224
QY 368 SGNCGLYYSSGWWFDACLSANLNGKYYHOKYRGVR-NGIFWGTWPGVSEAHPGGKYSFK 426
DB 225 C-KCSQMLTGGWFDACGPNLNGMYTPQONTNKGKIKWYWKG-----SGY--SLK 275
QY 427 EAKMIRPKHF 437
DB 276 ATTMIRPADF 286

RESULT 7
US-08-525-505A-4
; Sequence 4, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAeko
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-505A-4
Query Match 21.3%; Score 506; DB 1; Length 312;
Best Local Similarity 44.6%; Pred. No. 8.8e-39;
Matches 107; Conservative 25; Mismatches 88; Indels 20; Gaps 6;
QY 210 YKDCSDYIAIGKRSETYRVPDPKNSFEVYCDMETMGGWTVLQARLDGSGTFTWQ 269
DB 80 YADCSEIFNDGYKLSGFKIRPLQSPAEFVYCDMSD-GGGWTVIQRSDGSENERGK 138
QY 270 DYKAGFNL---RRFEFLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFL 326
DB 139 DYENGFNGFVQKHGEYWLGNLHLLTQEDYTLKIDLADFEKNSRYAQYKFKVGDENK 198
QY 327 KYRLHVGNYNGTAGDALRFNKH-----YNHDLKEFTTTPDKNDNDRYPCSGCGLYSSGWW 380
DB 199 FYELNIGEYSCTAGDSLAGNFHPEYOWWASHQRMKESTWDRDHDNY-EGNCAEEDQSGWW 257
QY 381 FDACLSANLNGKYYHOKYRG-VRNGIFWGTWPGVSEAHPGGKYSFKKAKMIRPKHFKP 439
DB 258 FNRCHSANLNGVYSGPYTAKTDNGIVVWTW-----HGWVYSLKSVVMKIRPNDFIP 309

RESULT 8
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-933-821-4

Query Match 21.2%; Score 505; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.2e-38;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;


```

RESULT 12
US-08-418-595-4
; Sequence 4, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/418,595
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. 1e-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADNDGDPGRN 112
DB 145 LRDVETQVLNQTSLRIQLLENSLSLYKLEKQLQOOTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNAKEEINVHLG-----RLEK-L 161
DB 192 SLL-----EHLKLEME---GKHKEELDTLKEEKNLQGLVTRQYIIIOELEKQL 237
QY 162 NLVNMNNIENYVDSKVANLTFVNSLDGKCSK---CPSQEQIQSRPVQHLYIKDCSDYYA 218
DB 238 NRATTNN--SVLQKQOLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADYQ 290
QY 219 IGRKRSSETRYV---TPDPKNSSEFYVCDMETGGGWTVLQARLDGSGTNRFTWQDYKAG 274
DB 291 AGFNKSGIYTIYINNMPEPK---KVFENMDVNGGWTVIQHRDGLDFQRCWKYKMG 346
QY 275 FGNLRREFWLGNDKHLTKSKEMILRIDLDFNGVELYALYDQFYVANEFLKYLRLHGVN 334
DB 347 FGNPSGEYWLGNFEFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKG 406
QY 335 YNGTAGDALRPNKHYNHDLKFTTTPDKDNDRYPSGNCGLYYSSGWWFDCALSANLNGKYY 394
DB 407 HTGTAGKQSSLIILH-GAD---FSTKADNDNCMC-KCALMLTGGWFWDFACGPNLNGMFY 461
QY 395 HQ-KYRGVNGIFWGTWPGVSEAHPPGKYSKSEKAKMMIRPKHF 437
DB 462 TAGONHGKLNIGIKWHYFKGPS-----YSLRSTTMMIRPLDF 497

RESULT 13
US-08-665,926-4
; Sequence 4, Application US/08665926

Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. 1e-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADNDGDPGRN 112
DB 145 LRDVETQVLNQTSLRIQLLENSLSLYKLEKQLQOOTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNAKEEINVHLG-----RLEK-L 161
DB 192 SLL-----EHLKLEME---GKHKEELDTLKEEKNLQGLVTRQYIIIOELEKQL 237
QY 162 NLVNMNNIENYVDSKVANLTFVNSLDGKCSK---CPSQEQIQSRPVQHLYIKDCSDYYA 218
DB 238 NRATTNN--SVLQKQOLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADYQ 290
QY 219 IGRKRSSETRYV---TPDPKNSSEFYVCDMETGGGWTVLQARLDGSGTNRFTWQDYKAG 274
DB 291 AGFNKSGIYTIYINNMPEPK---KVFENMDVNGGWTVIQHRDGLDFQRCWKYKMG 346
QY 275 FGNLRREFWLGNDKHLTKSKEMILRIDLDFNGVELYALYDQFYVANEFLKYLRLHGVN 334
DB 347 FGNPSGEYWLGNFEFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKG 406
QY 335 YNGTAGDALRPNKHYNHDLKFTTTPDKDNDRYPSGNCGLYYSSGWWFDCALSANLNGKYY 394
DB 407 HTGTAGKQSSLIILH-GAD---FSTKADNDNCMC-KCALMLTGGWFWDFACGPNLNGMFY 461
QY 395 HQ-KYRGVNGIFWGTWPGVSEAHPPGKYSKSEKAKMMIRPKHF 437
DB 462 TAGONHGKLNIGIKWHYFKGPS-----YSLRSTTMMIRPLDF 497

RESULT 14
US-08-348-492-4

Sequence 4, Application US/08348492
Patent No. 5879672
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,492
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 330B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELEFAX: (914) 347-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-492-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. le-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;

QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADNDGDPGRN 112
DB 145 LTDVETQVLNQTSLRIQLLENSLSTYKLEKQLQOOTNEILKIH-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNKAEINVLHG-----RLEK-L 161
DB 192 SLL-----EKKILEME---GKHREELDTLKEKENLQGLVTRQYIIQLEKQL 237
QY 162 NLVNMNNIENYDSKVANITFVNSLDGCKSK---CPSQEQIQSRPVQHLYIKDCSDYYA 218
DB 238 NRATTNN--SVLQKQQLLELMDTVHNLVNLCTKVELLKGKREEDKP-----FRDCADVQ 290
QY 219 IGRSSEYTRV---TPDPKNSFEYVCDMETGGTGVTLQARLDGSTNTRTWQDYKAG 274
DB 291 AGFNKSGIYTIINNPEPK-----KVCNMNVNGGGTIVIQHREDGSLDPQRMKEYKMG 346
QY 275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFENGVELYALDYQVYANFELKYLRLHGVN 334
DB 347 FGNPSGEYWLGNFPAITISQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYKLG 406
QY 335 YNGTAGDALLRNKHNHDLKFFTPDKDNDRYPSGNCGLYSSGWFDFACLSANLNGKYY 394
DB 407 HGTGAKQSSLLIH-CAD---FSTKADNDNCMC-KCALMLTGWGWFADACGPNLNGMFY 461

QY 395 HQ-KYRGVRNGIFWGTWPGVSEAHFPGYKSSFKKAKMMIRPKHF 437
DB 462 TAGQNHGKLGINKWYFKGPS-----YSLRSTTMMIRPLDF 497
RESULT 15
US-09-162-437-4
Sequence 4, Application US/09162437
Patent No. 6166185
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-4

Query Match 20.5%; Score 487; DB 3; Length 497;
Best Local Similarity 32.4%; Pred. No. le-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;

QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADNDGDPGRN 112
DB 145 LTDVETQVLNQTSLRIQLLENSLSTYKLEKQLQOOTNEILKIH-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNKAEINVLHG-----RLEK-L 161

Db 192 SLL-----EHKILEME---GKHKEELDTLKEKENLOGLVTRQTYIIQLEKOL 237
Qy 162 NLVNMNNTYVDSKVANLTFVYNSLDKCSK---CPSQEQIQSRPVQVHLYIKDCSDYYA 218
Db 238 NRATTNN--SVLQKQOLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADVQ 290
Qy 219 IGKRSSETYRV-----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTTWQDYKAG 274
Db 291 AGFNKSGIYTIYINNMEPK-----KVFCNMDVNGGGWTVIOHREDGSLDFQRGWKEYKMG 346
Qy 275 FGNLRREFWLGNDKTHLLTKSKEMILRIDLEFNGVELYALYDQFYVANEFLKYRLHVCN 334
Db 347 FGNPSGEYWLGNFEFATISQRYMLRIELMDWEGNRAYSQYDRFHIGNEKONYRDLKAG 406
Qy 335 YNGTAGDALRFNKHYNHDLKFEFTTPDKNDRYPSGNCGLIYSSGWWFDCACLSANLNGKYY 394
Db 407 HTGTAGKQSSLIH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFDCAGPSNLNGMEY 461
Qy 395 HQ-KYRGVYRNGIFWGTWPGVSEAHPGGYKSSPFKEAKMMIRPKHF 437
Db 462 TAGONHGKLGNGIKWHYFRGPS-----YSLRSTTMMIRPLDF 497

Search completed: February 27, 2001, 12:48:04
Job time: 30 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:09 ; Search time 19.29 seconds
(without alignments)
734.946 Million cell updates/sec

Title: US-09-442-143-2
Perfect score: 2378
Sequence: 1 MGLANWYWLSSAVLATYGF.....GYKSSFKEAKMIRPKHFKP 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB ID	Description
1	1853.5	77.9	432	1 FIBX_MOUSE P12804 mus musculus
2	511.5	21.5	463	1 FIBB_CHICK Q02020 gallus gall
3	481.5	20.2	453	1 FIBH_HUMAN P04469 homo sapien
4	479.5	20.2	477	1 FIBB_PETMA P02678 petromyzon
5	477.5	20.1	437	1 FIBG_HUMAN P02679 homo sapien
6	471	19.8	468	1 FIBB_BOVIN P02676 bos taurus
7	462	19.4	444	1 FIBG_BOVIN P12799 bos taurus
8	461	19.4	491	1 FIBB_HUMAN P02675 homo sapien
9	456	19.2	438	1 FIBG_XENLA P17634 xenopus lae
10	454.5	19.1	479	1 FIBB_RAT P14480 rattus norv
11	451	19.0	866	1 FIBB_HUMAN P02671 homo sapien
12	446	18.8	282	1 FIBA_PARPA P19477 parastichop
13	441	18.5	782	1 FIBA_RAT P06399 rattus norv
14	428.5	18.0	432	1 FIBG_PETMA P04115 petromyzon
15	427.5	18.0	741	1 FIBA_CHICK P14448 gallus gall
16	419	17.6	445	1 FIBG_RAT P02680 rattus norv
17	399	16.8	255	1 MFA4_HUMAN P55083 homo sapien
18	397.5	16.7	4289	1 TENX_HUMAN P22105 homo sapien
19	388	16.3	2201	1 TENA_HUMAN P24821 homo sapien
20	386.5	16.3	1746	1 TENA_PIG Q29116 sus scrofa
21	386	16.2	1808	1 TENA_CHICK P10039 gallus gall
22	358.5	15.1	641	1 FIB2_PETMA P33573 petromyzon
23	346.5	14.6	774	1 SCA_DROME P21520 drosophila
24	185.5	7.8	129	1 MFA4_BOVIN P55918 bos taurus
25	115	4.8	569	1 CISP_PLAFA P25805 plasmodium
26	114.5	4.8	485	1 NOMR_RAT Q62609 rattus norv
27	114.5	4.8	964	1 QOYL_CAEEL Q09560 caenorhabdi
28	114.5	4.8	1940	1 MYSE_RAT P12847 rattus norv
29	112	4.7	1940	1 MYSE_HUMAN P11055 homo sapien
30	107	4.5	1140	1 RA18_SCHPO P53692 schizosacch
31	106.5	4.5	1664	1 RPAL_YEAST P10964 saccharomyc
32	106	4.5	2245	1 MYSJ_DICTDI P54697 dictyosteli
33	105	4.4	362	1 RFL_AQUAE O67032 aquifex aeo

ALIGNMENTS				
RESULT	ID	FIBX_MOUSE	STANDARD;	PRT; 432 AA.
AC	P12804;			
DT	01-OCT-1989	(Rel. 12, Created)		
DT	01-OCT-1989	(Rel. 12, Last sequence update)		
DT	01-NOV-1997	(Rel. 35, Last annotation update)		
DE	PROTHROMBINASE PRECURSOR (FIBRINOGEN-LIKE PROTEIN) (CYTOTOXIC T-			
DE	LYMPHOCYTE SPECIFIC PROTEIN).			
GN	FIBLP OR FGL2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-CYTOTOXIC T-CELL;			
RX	MEDLINE=87175527; Pubmed=3550794;			
RA	Koyama T., Hall L.R., Hasegawa S., Saito H.;			
RT	"Structure of a cytotoxic T-lymphocyte-specific gene shows a strong			
RT	homology to fibrinogen beta and gamma chains.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	STRAIN=BALE/CJ; TISSUE=PERITONEAL MACROPHAGE;			
RX	MEDLINE=95333285; Pubmed=7609073;			
RA	Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,			
RA	Levy G.;			
RT	"Association of mouse fibrinogen-like protein with murine hepatitis			
RT	virus-induced prothrombinase activity.";			
RL	J. Virol. 69:5033-5038(1995).			
CC	-!- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.			
CC	-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC			
CC	T-CELLS.			
CC	-!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS			
CC	VIRUS STRAIN 3 (MHV-3).			
CC	-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF			
CC	THE BETA AND GAMMA CHAINS OF FIBRINOGEN.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M16238; AAA37624.1;			
DR	EMBL; M15761; AAA37624.1; JOINED.			
DR	EMBL; S78773; AAB34823.1;			
DR	PIR; A27447; A27447.			
DR	HSSP; P02671; IFZD.			
DR	MGD; MGI:103266; FGL2.			
DR	INTERPRO; IPR002181;			
DR	PFAM; PF00147; fibrinogen.C.1.			
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.			
KW	T-cell; Cytolysis; Blood coagulation; Signal.			

```

FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 PROTHROMBINASE.
FT DISULFID 206 235 BY SIMILARITY.
FT DISULFID 364 377 BY SIMILARITY.
FT CONFLICT 332 332 A -> G (IN REF. 2).
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CB4A782 CRC64;

Query Match 77.9%; Score 1853.5; DB 1; Length 432;
Best Local Similarity 77.7%; Pred. No. 3.4e-119;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

Qy 1 MCLANWYLSNAVLATYGLVANNETEBIKDERAKDVCVRLESRGKCEEAGECYPQVS 60
Db 1 MRLPGWLWLSAVLAACR-AVEEHLNTEGLEDAQAACPARLEGSGRC-EGSQCPFLT 58
Qy 61 LPPLTIQLPKFSTEEVFKEQNLKEIYVNSLKKSCODCKLOADDNGDPRGNLLLPSTG 120
Db 59 LPTLIQLPRQLGSWEELVKEVTLKEAVDSLKSKSCODCKLOADDHRDPGGNG----GNG 114
Qy 121 APGEVGNRVRESEVANKLSSELNAKEEINVLHGRLEKLNLVNMMNIENYVDSKVANL 180
Db 115 AE-TAEDSRVQESQVKNLSSELNAKDQIOGLQGRLETLHLVNNNNIENYVDKNVANL 173
Qy 181 TFVNSLDGKSKCPSEQIOQSRPOVHLLYKDCSDYIAGKRSSEYRVTDPKNSSEFV 240
Db 174 TVVNSLDGKSKCPSEQHMQSQVQHLHYKDCSDHYVLGRSSGAYRVTDPDRNSSFEV 233
Qy 241 YCDMETGSGWTVLQARLDGSTNFTWQDYKAGFNLREFWLGNDKTHLLTKSEMIL 300
Db 234 YCDMETGSGWTVLQARLDGSTNFTREWQDYKAGFNLREFWLGNDKTHLLTKSEMIL 293
Qy 301 RIDLEDFNGVELYALYDQFYVANEFLKYLHVGNYGTAGDALRFNKNHDLKFFTTTPD 360
Db 294 RIDLEDFNGLYALYDQFYVANEFLKYLHVGNYGTAGDALRFNKNHDLRFFTTTPD 353
Qy 361 KNDRYPSGNCGLYSSGWWFDCLSANLNGYKHQYKRGVNRGIFWGTWPGVSEAHPGG 420
Db 354 RNDRYPSGNCGLYSSGWWFDCLSANLNGYKHQYKRGVNRGIFWGTWPGINQAQPGG 413
Qy 421 YKSSPEKAKMIRPKFKP 439
Db 414 YKSSPEKAKMIRPKFKP 432

RESULT 2
FIBB_CHICK STANDARD; PRT; 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE-91182745; PubMed-2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site.";
RL Biochemistry 30:3290-3294(1991).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

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CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M58514; AAA48770.1; -
CC PIR; A38463; A38463.
CC HSSP; P02675; 1FZB.
CC INTERPRO; IPR002181; -
CC PFAM; PF00147; fibrinogen_C; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfatation.
CC FT NON_TER 1 1 FIBRINOPEPTIDE B.
CC PEPTIDE <1 17 FIBRINOPEPTIDE B.
CC CHAIN 18 463 FIBRINOGEN BETA CHAIN.
CC MOD_RES 5 5 SULFATATION (BY SIMILARITY).
CC SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
CC FT FIBRINOPEPTIDE B).
CC FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
CC FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
CC FT DISULFID 205 289 BY SIMILARITY.
CC FT DISULFID 215 244 BY SIMILARITY.
CC FT DISULFID 397 410 BY SIMILARITY.
CC FT CARBOHYD 367 367 N-LINKED (GLCNAC... ) (POTENTIAL).
CC SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 21.5%; Score 511.5; DB 1; Length 463;
Best Local Similarity 30.4%; Pred. No. 8.1e-28;
Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;

Qy 31 KDERAKDVCVRLESRGK-----EEAGE-CPYQVSLPPLTIQLPKQFSRIEVEFKEVN- 84
Db 51 QDKQAMKGPPIYPDAGGCKHPDELGVLCPTGCE---LQTTLLKQKTYVPLVDLKDOR 107
Qy 85 -----LKEIVNSLKKSCODCKLOADDNGDPRGNLLLPSTGAPGEVGNRVRELE 134.
Db 108 VAKFSDTSTTMYQVYVNMIDNKLVTQKQKD-----NDIILSEVNTMELHYNVIR--D 159
Qy 135 SEVKNLSSELNAKEEINVLHGRLEKLNLVNMMNIENYVDSKVANLTFVNSLDGKSKC 194
Db 160 NLDNNIPSSLRVLRAVDSLHKKIQKL-----ENAIATQT-----DYCRSPC 201
Qy 195 PSQEQIQRSPVOHLHYKDCSDYIAGKRSSEYRVTDPKNSSEVYCDMETGSGWTVL 254
Db 202 -----VASCNIPVVGSECEDIYRKGETSEMYIIQDPPTTPYRVYCDMETDNGWTLI 256
Qy 255 QARLDGSTNFTWQDYKAGFNLNR-----EFWLGNDKIHLTKSEMILRID 303
Db 257 QNRDGSVNFGRADWEYKRGFGNIAKSGGKCYCDTPCEYWLGNDKISQLTGKIGTKVLIE 316
Qy 304 LEDPNGVELYALYDQFYVANEFLKYLHVGNYGTAGDALR--FNKHYN-----HDLK 354
Db 317 MEDWNGDKVSLYGGFTIHNEGNYQLSVSNYKGNAGNALMEGASQLYGNRTMTIHNGM 376
Qy 355 FFTPDPKDNRY-----PSGNCGLYSSGWWFDCLSANLNGKY-----HQYRGNV 403
Db 377 YFSTYDRNDGWLTTDPKQCKSKEDGGWTFNRCHAANPNRGYWGTYSWDMAKHGTD 436
Qy 404 GIFWGTWPGVSEAHPGGYKSSFKKAKMIRP 434

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Db 437 GIVMNMWKG-----SWY---SMKKMSMKIRP 459

RESULT 3

FIBH_HUMAN STANDARD; PRT; 453 AA.

AC P04469; P04470;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA').

GN FGG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85252774; PubMed=2990550;

RA Rixon M.W., Chung D.W., Davie E.W.;

RT "Nucleotide sequence of the gene for the gamma chain of human fibrinogen.";

RL Biochemistry 24:2077-2086(1985).

RN [2]

RP CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.

RX MEDLINE=81054908; PubMed=6933547;

RA Wolfenstein-Todel C., Mosesson M.W.;

RT "Human plasma fibrinogen heterogeneity: evidence for an extended carboxyl-terminal sequence in a normal gamma chain variant (gamma').";

RL J. Biol. Chem. 259:12826-12830(1984).

RN [4]

RP SEQUENCE OF 411-453.

RX MEDLINE=82068993; PubMed=7306501;

RA Wolfenstein-Todel C., Mosesson M.W.;

RT "Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant (gamma').";

RL Biochemistry 20:6146-6149(1981).

RN [5]

RP SULFATATION.

RX MEDLINE=91369960; PubMed=1892842;

RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;

RT "Recombinant human fibrinogen and sulfation of the gamma' chain.";

RL Biochemistry 30:9414-9420(1991).

CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -!- ALTERNATIVE PRODUCTS: THIS CHAIN DIFFERS FROM THE GAMMA-A CHAIN AT RESIDUES 434-437 FOLLOWED BY 16 ADDITIONAL RESIDUES OF THE CARBOXYL END. THESE DIFFERENCES ARE PRODUCED BY AN ALTERNATE SPLICING OF THE MRNA IN WHICH THE EIGHTH (LAST) INTRON IS NOT REMOVED.

CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS.

CC -!- MISCELLANEOUS: THE GAMMA-B CHAIN IS PRESENT IN ABOUT 10% OF THE FIBRINOGEN MOLECULES IN PLASMA BUT ABSENT FROM THOSE IN THE PLATELETS.

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CC -----

DR EMBL; M10014; AAB59530.1; -

DR EMBL; X02415; -; NOT_ANNOTATED_CDS.

DR EMBL; K02569; AAB52430.1; -

DR PIR; A03126; FGHUGB.

DR HSPP; P02679; 1FZB.

DR MIN; 134850; -

DR INTERPRO; IPR002181; -

DR PFAM; PF00147; fibrinogen_C; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

KW Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma;

KW Alternative splicing; Sulfatation; Signal.

FT SIGNAL 1 26

FT CHAIN 27 453 FIBRINOGEN GAMMA-B CHAIN.

FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .).

FT DISULFID 34 34 INTERCHAIN (WITH C-35').

FT DISULFID 35 35 INTERCHAIN (WITH C-34').

FT DISULFID 45 45 INTERCHAIN (WITH C-110 IN BETA).

FT DISULFID 49 49 INTERCHAIN (WITH A-64 IN ALPHA).

FT DISULFID 161 161 INTERCHAIN (WITH C-227 IN BETA).

FT DISULFID 165 165 INTERCHAIN (WITH C-180 IN ALPHA).

FT DISULFID 179 208

FT DISULFID 352 365

FT CA_BIND 341 355

FT SITE 400 422

FT

FT POLYMERIZATION SITE, BINDING TO THE AMINO END OF ALPHA-CHAIN OF ANOTHER FIBRIN MONOMER.

FT CROSS-LINK TO 432-LYS AND 424-GLN.

FT CROSS-LINK TO 432-LYS AND 424-GLN.

FT SULFATATION (PROBABLE).

FT R -> Y (IN REF. 4).

FT Y -> R (IN REF. 4).

SQ SEQUENCE 453 AA; 51496 MW; FA647C5E85A2013A CRC64;

Query Match 20.2%; Score 481.5; DB 1; Length 453;

Best Local Similarity 29.3%; Pred. No. 8.7e-26;

Matches 139; Conservative 59; Mismatches 177; Indels 99; Gaps 17;

QY 8 WLSSAVLATYGLVYVANNETEETEEKDRAKDCVPVRLESRGKCEAGECPYQVSLPLTIQ 67

Db 19 FLSTCVV-----YVATRDNCILDERGSCYPT-----TCGIADFLSTYQTK 61

QY 68 LPKQFSRIEVEFKEVQNLKEIVNSLKSCQCKLQADGDPGRNGLLPSTGAPGEVGD 127

Db 62 VDKDLQSLIEDILHQVENKTSVKQLIKA-----IQLTYNPDESSKPNMIDATLKSRLM 116

QY 128 NRVELESEVKNLSSELKNAKEEINLVHGRLEKLVNMMNIENVYDVKVANLFTVNSL 187

Db 117 EETMKYEASILTHDSSTIRYLOE-----IYNSNN-----QKIVNLKEKVAQL 157

QY 188 DGKCSKPSQBOIQSRPVQHLIYKDCSDYVYAIKGRSSSETYRVTDPKNSSEVYCDMETM 247

Db 158 EAQCOE-PCKDTVQ---IHDITGDCQDIANKGAKQSGLYFIKPKLANKQOFLVYCEIDGS 213

QY 248 GGGVTVLQARLDGSTNFTRTWQDYKAGFNL-----RREFWLGNDKIHLLTSKEM--ILR 301

Db 214 GNGWTFQKRLDGSVDFFKNNIQYKEGHLSPGTCTTEFWLGNEKIHLLTSQSAIPYALR 273

QY 302 IDLEDFNGVELYALDYQFVYANFELKYLHVGNV-NGTAGDAL-RFNKHYNHLKFFT-- 357

Db 274 VELEDWNGRTSTADYAMFKVGPEDAKYRLTYAYFAGGDAGDAFDGDFGDPDSKFFTS 333

QY 358 -----TPDKNDYRPSGNCGLYSSGWFWDACLSANLNGKYH-----QKYRGVNG 404

FT	DISULFID	212	212	INTERCHAIN (WITH THE ALPHA CHAIN)
FT	FT			(BY SIMILARITY).
FT	DISULFID	216	216	INTERCHAIN (WITH THE GAMMA CHAIN)
FT	FT			(BY SIMILARITY).
FT	DISULFID	220	304	BY SIMILARITY.
FT	DISULFID	230	259	BY SIMILARITY.
FT	DISULFID	412	425	BY SIMILARITY.
FT	SEQUENCE	477 AA;	54270 MW;	B8A95E7E32D09D18 CRC64;

Query Match	20.2%;	Score 479.5;	DB 1;	Length 477;	
Best Local Similarity	29.2%;	Pred. No. 1.3e-25;			
Matches 131;	Conservative	66;	Mismatches 138;	Indels 113;	Gaps 15;

QY	29	EIKDERAKDVCVRLSRGKCEAGECPYQVSLPLTJQLPKQFSRIEVEFKEVQNLKEI	88
DB	100	ELRELLKQDPVR-----YKISMLK-----QNLTYF	126
QY	89	VNSLKSKQCDCKLQADDNGDPRNGLLPLSTGAPGVDGNRVRELESEVNSKLSELKNAK	148
DB	127	INSPDR-----MASDSNTLKQN-----VQTLRRRLNSRSSTHVNAQ	162
QY	149	EEINVLHGRLEKLNLMVNNTENTYDSKVANLTFVNSLDGKCSK----CFSQEQIQSRP	204
DB	163	KEI-----ENRYKEVKI-----RIESTVAGSLRGSVLEHLRAKMORMEPAIKTQKELCSAP	215
QY	205	-----VOHLLYKDCDYAIGKSSERYVTPDPKNSSEFVCDMETMGGWTVLOARL	258
DB	216	CTVNCRPVVSVMCEDIYRNGGRTSEAYIOPDLFSEPKYVFCDMESHGSGWTVVQNRV	275
QY	259	DGSTNFTRTWQDYKAGFGNLR-----REFWLGNDKIHLLTSKEMILRIDLDF	307
DB	276	DGSSNFARDWNTYKAERGNIAFGNGKSCINIPGEWLGTKTVHOLTQHTQOVLFDMSDW	335
QY	308	NGVELYALYDQFYVANFELKYRLHVGNVNGTAGDAL-----RPNKHYN-HDLKFTTT	358
DB	336	EGSSVYAQYAFRPENEAQQYRLWVEDYSGNAGNALLEGATQLMGDNRTMTIHNGMQFST	395
QY	359	PKDKNDRY-----PSNGCLYYSGGWPFDACLSANLNGKY-----HOKYRGVRNGIFW	407
DB	396	FDRDNDWNPDPKTHCSREDAGGWYNRCHAANPNRGYWGGIYTKEQADYGTDDGVVW	455
QY	408	GTWPGVSEAHPPGYKSSFKFEAKMMIRPK	435
DB	456	MNWKG-----SWY--SMRQAMKLRPK	475

RESULT 5			
FIBG HUMAN			
ID FIBG HUMAN	STANDARD;	PRT;	437 AA.
AC	P02679;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	13-AUG-1987	(Rel. 05, last sequence update)	
DT	15-JUL-1999.	(Rel. 38, last annotation update)	
DE	FIBRINOGEN GAMMA-A CHAIN	PRECURSOR.	
GN	FGG.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RN	{1}		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=8525774;	PubMed=2990550;	
RA	Rixon M.W., Chung D.W., Davie E.W.;		
RT	"Nucleotide sequence of the gene for the gamma chain of human		
RT	fibrinogen."		
RL	Biochemistry 24:2077-2086(1985).		
RN	{2}		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=83283434;	PubMed=6688357;	
RA	Chung D.W., Chan W.-Y., Davie E.W.;		
RT	"Characterization of a complementary deoxyribonucleic acid coding for		
RT	the gamma chain of human fibrinogen."		
RL	Biochemistry 22:3250-3256(1983).		

RN [13]
 RP SEQUENCE OF 27-437.
 RX Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RA "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [4]
 RP SEQUENCE OF 75-286 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=92119334; PubMed=1685103;
 RA Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene.";
 RL DNA Seq. 1:419-422(1991).
 RN [5]
 RP SEQUENCE OF 285-437 FROM N.A.
 RX MEDLINE=85030379; PubMed=602346;
 RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
 RA Crabtree G.R.;
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen.";
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [6]
 RP SEQUENCE OF 209-270 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Imam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [7]
 RP REVIEW, AND DISULFIDE BONDS
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [8]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takeda T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.K., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (In) Magnusson S., Ottesen M., Folmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [10]
 RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE=83231465; PubMed=6860649;
 RA Hoeprich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation.";
 RL Biochemistry 22:2049-2055(1983).
 RN [11]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [12]
 RP POLYMERIZATION SITE.
 RX MEDLINE=85014892; PubMed=6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [13]

RP POLYMERIZATION SITE.
 RX MEDLINE=81142375; PubMed=6451630;
 RA Olexa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site.";
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [14]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE=84203545; PubMed=6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain.";
 RL Biochemistry 23:1767-1774(1984).
 RN [15]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE=84185664; PubMed=6325435;
 RA Plow E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets.";
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [16]
 RP CALCIUM-BINDING SITE.
 RX MEDLINE=85261382; PubMed=3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by terbium fluorescence.";
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=97169449; PubMed=9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen.";
 RL Structure 5:125-138(1997).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=97352771; PubMed=9207064;
 RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
 RT "The primary fibrin polymerization pocket: three-dimensional
 RT structure of a 30-kDa C-terminal gamma chain fragment complexed with
 RT the peptide Gly-Pro-Arg-Pro.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
 RX MEDLINE=97472408; PubMed=9333233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment Double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [22]
 RP VARIANT ASAH1.
 RX MEDLINE=89214687; PubMed=2496144;
 RA Yamazumi K., Shimura K., Terukina S., Takahashi N., Matsuda M.;
 RT "A gamma methionine-310 to threonine substitution and consequent N-
 RT glycosylation at gamma asparagine-308 identified in a congenital
 RT dysfibrinogenemia associated with posttraumatic bleeding, fibrinogen
 RT Asahi.";
 RL J. Clin. Invest. 83:1590-1597(1989).


```

Db 321 GDDSSDKFTSHGMOFTWDSNDXY-DGNCAEQVIGIWMNKCHAGHNGVYQGGTY 379
QY 396 ---QXYRGVRNGIFWTGPGVSEAHGGYKS---SPKEAKMMIRP 434
Db 380 SKTSTPNGYDNGIWIATW-----KSRWYSMKKTKTKIIP 413

RESULT 8
FIBB_HUMAN
ID FIBB_HUMAN STANDARD; PRT; 491 AA.
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR.
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic
RL deoxyribonucleic acid for the beta chain of human fibrinogen.";
RL Biochemistry 22:3244-3250(1983).
RN [3]
RP SEQUENCE FROM N.A.
RA Chung D.W., Harris J.E., Davie E.W.;
RL (In) Chien S. (eds.);
RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
RL Plenum Press, New York (1991).
RN [4]
RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RL structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [5]
RP SEQUENCE OF 31-491.
RX MEDLINE=79124640; PubMed=420779;
RA Watt K.W.K., Takagi T., Doolittle R.F.;
RT "Amino acid sequence of the beta chain of human fibrinogen.";
RL Biochemistry 18:68-76(1979).
RN [6]
RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [7]
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=871146483; PubMed=3029722;
RA Huber P., Dalmon J., Courtols G., Laurent M., Assouline Z.,
RA Marguerie G.;
RT "Characterization of the 5'-flanking region for the human fibrinogen
RL beta gene.";
RL Nucleic Acids Res. 15:1615-1625(1987).
RN [8]
RP SEQUENCE OF 31-44.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).

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RN [9]
RP REVIEW, AND DISULFIDE BONDS.
RX MEDLINE=83254370; PubMed=6575689;
RA Henschen A., Lottspeich F., Kehl M., Southan C.;
RT "Covalent structure of fibrinogen.";
RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=77245999; PubMed=891553;
RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
RT "Primary structure of human fibrinogen. Characterization of
RL disulfide-containing cyanogen-bromide fragments.";
RL Eur. J. Biochem. 77:595-610(1977).
RN [11]
RP DISULFIDE BONDS.
RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friezner S.J.;
RT "The structures of fibrinogen and fibrin.";
RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
RL Neurath H. (eds.);
RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
RL Pergamon Press, New York (1978).
RN [12]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX MEDLINE=97472408; PubMed=9332333;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RL crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RL different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [16]
RP VARIANT BALTIMORE-2.
RX MEDLINE=89058942; PubMed=3194892;
RA Schneizer C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
RL structural studies of fibrinogen Baltimore II.";
RL Thromb. Res. 52:173-177(1988).
RN [17]
RP VARIANT ISE.
RX MEDLINE=91208409; PubMed=2018836;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RA Asakura S., Shirakawa S.;
RT "A new congenital abnormal fibrinogen Ise characterized by the
RL replacement of B beta glycine-15 by cysteine.";
RL Blood 77:1958-1963(1991).
RN [18]
RP VARIANT NAPLES.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT "Molecular basis of fibrinogen Naples associated with defective
RL thrombin binding and thrombophilia. Homozygous substitution of B beta
RL 68 Ala-->Thr.";
RL J. Clin. Invest. 90:238-244(1992).
RN [19]

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RP VARIANTS IJMUDEN AND NIJMEGEN.
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens IJmuden (B beta Arg14-->Cys) and Nijmegen (B
 RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [20]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COLLS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -!- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC
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 CC
 DR EMBL; J00129; AAA52429.1; -;
 DR EMBL; J00131; AAA98115.1; -;
 DR EMBL; J00130; AAA98115.1; JOINED.
 DR EMBL; J00132; AAA98116.1; -;
 DR EMBL; J00133; -; NOT_ANNOTATED_CDS.
 DR EMBL; X05018; CAA28674.1; -;
 DR EMBL; M64983; AAA18024.2; -;
 DR EMBL; M26877; AAA52445.1; -;
 DR EMBL; M26876; AAA52445.1; JOINED.
 DR PIR; B43568; FGHUB.
 DR PDB; 1FZA; 03-DEC-97.
 DR PDB; 1FZB; 03-DEC-97.
 DR PDB; 1FZC; 14-OCT-98.
 DR PDB; 1FEZ; 08-JUN-99.
 DR PDB; 1FEF; 08-JUN-99.
 DR PDB; 1FEZG; 08-JUN-99.
 DR SWISS-2DPAGE; P02675; HUMAN.
 DR MIM; 134830; -;
 DR INTERPRO; IPR002181; -;
 DR PFAM; PF00147; fibrinogen_C; 1.
 Query Match 19.4%; Score 461; DB 1; Length 491;
 Best Local Similarity 28.7%; Pred No. 2.4e-24;
 Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps 14;
 QY 27 TTEIKDERAKDVCPRVLRSGKCEAGE-----CPYQVSLPPLTIQLPKOF-SRIEEVFK 80
 Db 81 TQKKVERKAPDA-----GGCLHADPDGLVLCPTGCGQLQEAALLQOERPIRNSVDLNN 132

QY 81 EVQNLKEIVNS-----LKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVREL 133
 Db 133 NVEAVSQTSSSSFOYMYLLKDLWKQRQKQVDN----- 165
 QY 134 ESEVNLKSELKNAKEEINVLHGRLEKLNLMNMIENIVDSKVANLTFVNSLDGCKSK 193
 Db 166 ENVVNEYSSE-----LEKHQLYIDETVNSNIPITNLRLVRLSILENLSRKIQK 211
 QY 194 CPSQEQIQ-----SRPQHLIYKDCSDYYAIGKRSSSTYRYVTPDPKNSSEFVCD 243
 Db 212 LESDVAQMEYCRTPCTVSCNIPVVSGRECEIIRKGETSEMYLIQDSSVVKPRVYCD 271
 QY 244 METGGGTVTLQARLDGSTNFTRTWQDYKAGFGN-----LRREFWLGNKDIHL 291
 Db 272 MNTGNGTVTLQNRQDGSVDFGRKWDVPYKQGNVATWTDGKNYKGLPGEYWLGNKDISQ 331
 QY 292 LTKSKEMILRLDLEDFNOVELYALDYQYVANEFUKYRLHGVNGYNGTAGDALR----- 344
 Db 332 LTRMGPTTELLIEMEDWKGVKAHYGGFTVQNEANKYQISVKNKYRGTAGNALMDGASQLM 391
 QY 345 -FNKHYN-HDLKFFTPDKNDRY-----PSGNCGLIYSSGWFDFACLANLNGKY----- 394
 Db 392 GENRTMTHNGMFFSTYDRDNDGWLTSDPKQCKSKEDGGGWMYNRCHAANPNGRYWGQ 451
 QY 395 ---HQYRGVNRNGIFWGTWPGVSEAHPGYKSSFKKAKMIRP 434
 Db 452 YTWDAKHGTDGDDGVVWNNK-----SWY--SMRKMSMKIRP 486
 RESULT 9
 ID FIBG_XENLA STANDARD; PRT; 438 AA.
 AC P17634;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIBRINOGEN GAMMA CHAIN PRECURSOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90241882; PubMed=2334684;
 RA Pastori R.L., Moskaitis J.E., Smith L.H. Jr., Schoenberg D.R.;
 RT "Estrogen regulation of Xenopus laevis gamma-fibrinogen gene
 RT expression.";
 RL Biochemistry 29:2599-2605(1990).
 RN [2]
 RP SEQUENCE OF 1-58 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=91146806; PubMed=2289632;
 RA Bhattacharya A., Shepard A.R., Moser D.R., Holland L.J.;
 RT "Isolation and characterization of cDNA clones for the gamma subunit
 RT of Xenopus fibrinogen, the product of a coordinately regulated gene
 RT family.";
 RL Mol. Cell. Endocrinol. 72:213-220(1990).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC
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FT DISULFID 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 219 BY SIMILARITY.
FT DISULFID 229 BY SIMILARITY.
FT DISULFID 238 BY SIMILARITY.
FT CARBOHYD 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 28 LSI -> ILS (IN REF. 3).
FT CONFLICT 30 L -> O (IN REF. 5).
FT CONFLICT 439 S -> T (IN REF. 5).
FT CONFLICT 441 S -> T (IN REF. 5).
FT CONFLICT 445 S -> A (IN REF. 5).
FT CONFLICT 467 R -> K (IN REF. 5).
FT CONFLICT 475 V -> F (IN REF. 5).
SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E0EC0 CRC64;

Query Match 19.1%; Score 454.5; DB 1; Length 479;
Best Local Similarity 31.2%; Pred. No. 6.4e-24;
Matches 116; Conservative 46; Mismatches 135; Indels 75; Gaps 10;

QY 128 NRVRELESEVN-----KLSSELKNAKEEINVLHGRLEKLNLM 166
Db 113 NSIAELNSNINSVYETSSVTFQYFLLLKDMWKKQAQVKDENVINEYSILEDQKLYID 172
QY 167 NNIEYVDSKVANLTFVYVNSLDGKCKSPQSQIQSR-----PVQHLYIKDCS 214
Db 173 ETVNDNIPNLRLVLSILEDLSKQKLESIDISATEYCHTPTVCNCPV--VSKECE 230
QY 215 DYIAIGKRSSEYRYTPDPKSSFEVYCDMETMGGWTVLQARLDGSGTFTWQDYKAG 274
Db 231 EIIRKGGTSEMVLQPTSSKPYRYCDMTKENGWTVIQNRQDGSVDFGRKWDPPYKKG 290
QY 275 FGN-----LRREFWLGNDKIHLTFSKEMILRIDLEDNGVELYALYDQFYVA 322
Db 291 FGNATNEDTKYCYGLPEYWLGNLKDLSQLTRIGPTTELLIEMEDKGRVKAHYGFTVQ 350
QY 323 NEFLKRLHVGNYNGTAGDALR-----FNKHYN-HDLKFFTPDKNDRY----PSG 369
Db 351 TEANKYQSVNKKYKTAGNALMEGASQLVGENRTWTHNGMFYSYDRNDGQWVTDPRK 410
QY 370 NGLYYSSGWFWFACLSANLKKYY-----HQYRGVNRGIFWGTWPGVSEAHPGGYK 422
Db 411 QCSKEDGGWYVNRCHAANPNRGYWGGLYSWDMSKHGTDGCVVWNWKG-----SWI- 463
QY 423 SSFKEAKMIRP 434
Db 464 -SMRRMSMKIRP 474

RESULT 11
FIBA_HUMAN
ID AC P02671; STANDARD; PRT; 866 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.M., Griendinger G.
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits.";
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).

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RA Chung D.W., Griendinger G.;
RL (In) Ebert R.F. (eds.);
RL Index of variant human fibrinogens, pp.13-24, CRC Press,
RL Boca Raton (1994).
RN [3]
RP SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
RC TISSUE=LIVER;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RN [4]
RP Adv. Exp. Med. Biol. 281:39-48(1990).
RX SEQUENCE FROM N.A. (ALPHA FORM).
RP MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [5]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=83283432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen.";
RL Biochemistry 22:3237-3244(1983).
RN [6]
RP SEQUENCE OF 20-629.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [7]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX MEDLINE=80088231; PubMed=518846;
RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence.";
RL Biochemistry 18:5410-5416(1979).
RN [8]
RP SEQUENCE OF 110-156 FROM N.A.
RX MEDLINE=84069777; PubMed=6689067;
RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT "Isolation and characterisation of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen.";
RL Nucleic Acids Res. 11:7427-7434(1983).
RN [9]
RP SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
RX MEDLINE=83254384; PubMed=6575700;
RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT "Cloning of fibrinogen genes and their cDNA.";
RL Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN [10]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [11]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80088230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human
RT fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).

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15-JUL-1999 (Rel. 38, Last annotation update)
 FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
 Parastichopus parvianensis (Sea cucumber).
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Holothuroidea; Aspidochirotrata; Aspidochirotrata; Stichopodidae;
 Parastichopus.
 [1]
 SEQUENCE FROM N.A.
 TISSUE=SOFT TISSUES;
 MEDLINE=90192754; PubMed=2315305;
 Xu X., Doolittle R.F.;
 "Presence of a vertebrate fibrinogen-like sequence in an echinoderm.";
 Proc. Natl. Acad. Sci. U.S.A. 87:2097-2101(1990).
 -!- SIMILARITY: RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA
 CHAINS OF FIBRINOGEN.

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 EMBL; M31326; AAA29962.1; -
 PIR; A35084; A35084.
 HSSP; P02671; 1FZD.
 INTERPRO; IPR002181; -
 PFAM; PF00147; fibrinogen_C; 1.
 PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW SIGNAL.
 FT CHAIN 1 24 FIBRINOGEN-LIKE PROTEIN A.
 FT DISULFID 70 101 BY SIMILARITY.
 FT DISULFID 224 240 BY SIMILARITY.
 SQ SEQUENCE 282 AA; 32280 MW; 07326C8865B7D3A2 CRC64;

 Query Match 18.8%; Score 446; DB 1; Length 282;
 Best Local Similarity 43.2%; Pred. No. 1.2e-23;
 Matches 99; Conservative 33; Mismatches 75; Indels 22; Gaps 9;
 QY 211 KDCSDYY--AIGKR-SSEYTRVTPDPKNSFEVYCDMETMGGWTLQARLDGTSNFT 267
 DB 68 RCYDILQSCSQSPSGQYQTPDQGN-LIKVYCDMETDEGWTVFQRIDGTINFYRS 126
 QY 268 WQYKAGFNLREFFWLGNDKIHLLTKSEMILRLDLPNGVELYALYDOFYVANEFLK 327
 DB 127 WSYQTGFGNLTAEFLGNDNIHLTSQGDYELRVELNNTLGNHYAKYKFRIGDSFSE 186
 QY 328 YRLHVGNYNTAGDALRFNKHYNHDLKFTTPDKNDPRPSGNCGLYSSG---WVFDAC 384
 DB 187 YLLVLGAYSGTAGDSLAY-----HNTPRFSTYDNDNDVY-SINCASHSSYGRGAWYKSC 240
 QY 385 LSNANLNGKYHKGVRNGIFWGTWPGVSEAHPGYKSFKEAKMMIR 433
 DB 241 LLSNLNGQY--DYSGAPS-IYWSYLPQNDQIP-----FAEMKLRN 280
 RESULT 13
 FIBA_RAT
 ID FIBA_RAT STANDARD; PRT; 782 AA.
 AC P06399;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
 GN FGA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA Fu Y., Cao Y., Hertzberg K., Grieninger G.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ALPHA FORM).
 RX MEDLINE=86011580; PubMed=4046033;
 RA Crabtree G.R., Comeau C.M., Fowlkes D.M., Fornace A.J. Jr.,
 RA Malley J.D., Kant J.A.;
 RA "Evolution and structure of the fibrinogen genes. Random insertion of
 RT introns or selective loss?";
 RL J. Mol. Biol. 185:1-19(1985).
 RN [3]
 RP SEQUENCE OF 20-36.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 458-550 FROM N.A. (ALPHA FORM).
 RC STRAIN=WISTAR; TISSUE=LIVER;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotti A.-M., Taroux P., Duquet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 liver regeneration.";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL MODULE.
 CC DIVERGING FROM THIS MODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL MODULE TO THE DISTAL MODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
 CC PREDOMINANT FORM.
 CC -!- PTM: THE ALPHA CHAIN IS NOT GLYCOSYLATED.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@sib-sib.ch).
 CC -----
 EMBL; X86561; CAA60264.1; -
 EMBL; X86561; CAA60263.1; -
 EMBL; M35601; AAA41158.1; -
 PIR; A03119; FGRTA.
 HSSP; P02671; 1FZD.
 INTERPRO; IPR002181; -
 PFAM; PF00147; fibrinogen_C; 1.
 PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Blood coagulation; Plasma; Platelet; Signal; Alternative splicing.
 FT SIGNAL 1 19 FIBRINOPEPTIDE A.
 FT PEPTIDE 20 36 FIBRINOGEN ALPHA-E CHAIN.
 FT CHAIN 20 782 CLEAVAGE (BY THROMBIN); RELEASE
 FT SITE 36 37 FIBRINOPEPTIDE A).
 FT DISULFID 48 48 INTERCHAIN (WITH C-48') (BY SIMILARITY).
 FT DISULFID 56 56 INTERCHAIN (WITH BETA) (BY SIMILARITY).
 FT DISULFID 65 65 INTERCHAIN (WITH C-49 IN GAMMA)
 FT (BY SIMILARITY).
 FT DISULFID 69 69 INTERCHAIN (WITH BETA) (BY SIMILARITY).

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FT DISULFID 181 INTERCHAIN (WITH C-165 IN GAMMA)
FT DISULFID 185 (BY SIMILARITY).
FT DISULFID 185 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT DISULFID 434 BY SIMILARITY.
FT VARSPLIC 547 DCDD -> GIHA (IN ISOFORM ALPHA).
FT VARSPLIC 551 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 30 EAGD -> DEGAG (IN REF. 3).
FT CONFLICT 140 Q -> E (IN REF. 2).
FT CONFLICT 212 D -> E (IN REF. 2).
FT CONFLICT 270 ASRGDLP -> LRREIYQ (IN REF. 2).
FT CONFLICT 473 S -> K (IN REF. 4).
SQ SEQUENCE 782 AA; 85685 MW; 744834DAE76D34C2 CRC64;

Query Match 18.5%; Score 441; DB 1; Length 782;
Best Local Similarity 31.0%; Pred. No. 1e-22;
Matches 118; Conservative 61; Mismatches 116; Indels 86; Gaps 16;

QY 125 VGNVRVRESEVKNLSSELKNAKE--EINVH---GRLEKLNLMNMIENIYVDSKVAN 179
DB 413 LGNDGHEVVKV-VTSDGSDCGDGMGLGTHFSGRDLDSRMH-PELGSEFYDSRFGS 470
QY 180 LTFVNSLDGKCKPCSOEQIOSRPVOHL-TYKDCSDYIAGKRSEYRYVTPD----- 232
DB 471 LTSNFKFGSKTSDSDIFTDIEN-PSSHVPFSSSKTSTVTKQVTKSKYMADEAASEAH 529
QY 233 -----PRNSS-FEYICOMETMGGGWT 252
DB 530 QEGDTRTKGRARTMRCDDVLQTHPSGAONGIFSILPGSSKIFSYCQETSIGWL 589
QY 253 VLQARLDGNTFTWQDYKAGFNL-----RRFWLGNKXTHLLTKSEMILRIDLEFN 308
DB 590 LIOQMDGSLNFNRTWQDYKRGFGLNDKGEFGLGNDYLLHLLT-LRGSVLRLVEEDWA 648
QY 309 GVELYALYDQFYVANEFLKYLHLVGNVNGTAGDAL-----RFNKHYNHLKFFTPDKD 362
DB 649 GKEAYET-HFRVGEAEYALQVSSVQGTAGDALMEGSVEEGTEYTSNNQFSTFDR 707
QY 363 NDRYPSCNGLYISGWWFADACLSANLNGKYY-----HOKYRGVNRNGIFWGTWPGV 413
DB 708 ADQWEE-NCAEYVGGWVNSQANLNGIYYPGTYDPRNNSPYE-LENGVLWVPPFGA 765
QY 414 SEAHPGYKSFKEAKMIRP 434
DB 766 D-----YSLWAVRMKIRP 778

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RESULT 14

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FIBG_PETMA STANDARD; PRT; 432 AA.
AC P04115;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIBRINOGEN GAMMA CHAIN PRECURSOR.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85199776; PubMed=2581603;
RA Strong D.D., Moore M., Cottrell B.A., Bohonus V.L., Pontes M.,
RA Evans B., Riley M., Doolittle R.F.;
RT "Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and
RT general characterization.;"
RL Biochemistry 24:92-101(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC -1- POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

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CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
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CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K03049; AAA49362.1; .
DR PIR; A03129; FGLMGS.
DR HSSP; P02679; 1FIC.
DR INTERPRO; IPR002181; .
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 432 FIBRINOGEN GAMMA CHAIN.
FT DISULFID 32 32 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 42 42 INTERCHAIN (WITH THE BETA CHAIN)
FT DISULFID 46 46 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 158 158 INTERCHAIN (WITH THE BETA CHAIN)
FT DISULFID 162 162 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 178 207 BY SIMILARITY.
FT DISULFID 348 361 BY SIMILARITY.
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 432 AA; 49203 MW; B503979B296DFB24 CRC64;

Query Match 18.0%; Score 428.5; DB 1; Length 432;
Best Local Similarity 33.8%; Pred. No. 3.3e-22;
Matches 114; Conservative 46; Mismatches 132; Indels 45; Gaps 14;

QY 127 DNKRVRESEVKNLSSE--LKNAKEINVLHGRLEKLNLMNMIENIYVDSKVANLTFV 184
DB 90 DVRTREDAQIIKDSQKTVQKILEVRI-----LEQIGVSHDAQIOELSEMVRVNOQFVT 145
QY 185 N-----SLDGKCKPCSOEQIOSRPVQHLIYKDCSDYIAGKRSEYRYVTPDPKNSSF 238
DB 146 RLQQQLVDIRQTCR--SCQDTTANKISPITGKDCQVVDNGKDSGLYIKPLKAKQPF 203
QY 239 EYVCDMETMGGTWTVLQARLDGSTNFTWQDYKAGFG-----NLRREFWLGNDKIHLLTK 294
DB 204 LVFCEIEN-GNGWTVIQHRDGSVNFTRDQVSYREGFYGLAPLTLTTFEFLGNEKIHLLTG 262
QY 295 SKEMILRIDLEFNGVELYALYDQFYVANEFLKYLHLVGNV-NGTAGDAL-----RF 345
DB 263 QQAYRURIDLTWENTHRYADYGHFKLTPESEDEYRLFYSWYLDGDAGNAGDFDGDQ 322
QY 346 NKHYNHL-LKFFTPDKNDNDYPSGNGCLYISGWWFADACLSANLNGKYYH-QYRGV-- 401
DB 323 DKFYTHLGMLESTPERDNDKY-EGSCAQDQSGWMMNRCHAGHLNGKYFGNGYRKTDV 381
QY 402 ----RNGIFWGTWPGVSEAHPGYKSFKEAKMIRP 434
DB 382 EFPYDDGLIWTW-----HWRWY--SLKMTTMKLLP 410

RESULT 15
FIBG_CHKCK
ID FIBG_CHKCK STANDARD; PRT; 741 AA.
AC P14448;

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